GenCore version 5.1.8

OM protein - protein search, using sw model

Run on: May 15, 2006, 13:26:41 ; Search time 190 Seconds
(without alignments)
2594.647 Million cell updates/sec

Title: US-10-602-441-4
Perfect score: 5901
Sequence: 1 MTRAPRCPAVRSLLRSRYRE.....TILKAAADPALSTDFQTILD 1122

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5901	100.0	1122	2	AAY26579	Aay26579 Murine te
2	5901	100.0	1122	8	ADG90601	Adg90601 Murine TE
3	5854	99.2	1122	5	ABB06711	Abb06711 Mouse tel
4	4859	82.3	1152	8	ADG90609	Adg90609 TERT cons
5	4751	80.5	1128	7	ADD21416	Add21416 Golden ha
6	4751	80.5	1128	8	ADG90603	Adg90603 Hamster T
7	3505	59.4	1132	2	AAW46957	Aaw46957 Human tel
8	3505	59.4	1132	2	AAW90251	Aaw90251 Human cat
9	3505	59.4	1132	2	AAY28881	Aay28881 Human tel
10	3505	59.4	1132	2	AAY32090	Aay32090 Human tel
11	3505	59.4	1132	2	AAY43621	Aay43621 A human t
12	3505	59.4	1132	2	AAY26580	Aay26580 Human tel
13	3505	59.4	1132	4	AAG64859	Aag64859 Heart mus
14	3505	59.4	1132	4	AAG64329	Aag64329 Human pro
15	3505	59.4	1132	4	AAB99930	Aab99930 Human tel
16	3505	59.4	1132	4	AAB82765	Aab82765 Human tel
17	3505	59.4	1132	5	AAE29226	Aae29226 Human tel
18	3505	59.4	1132	5	AAU72735	Aau72735 Human tel
19	3505	59.4	1132	6	ABR42384	Abr42384 Human tel
20	3505	59.4	1132	6	ABR42063	Abr42063 Human tel
21	3505	59.4	1132	6	ABP56676	Abp56676 Human tel
22	3505	59.4	1132	6	ABR58045	Abr58045 Human tel
23	3505	59.4	1132	7	ADD21420	Add21420 Human TER
24	3505	59.4	1132	7	ADH72743	Adh72743 Human pro
25	3505	59.4	1132	8	ADG70114	Adg70114 hTERT pro
26	3505	59.4	1132	8	ADG90599	Adg90599 Human TER
27	3505	59.4	1132	8	ADI82172	Adi82172 Human tel
28	3505	59.4	1132	8	ADR70482	Adr70482 Human tel
29	3505	59.4	1132	9	ADY25759	Ady25759 Human tel
30	3505	59.4	1154	2	AAW61350	Aaw61350 Human tel
31	3505	59.4	1189	2	AAW47008	Aaw47008 Glutathio
32	3499	59.3	1285	2	AAW47000	Aaw47000 HIS tagge
33	3498	59.3	1132	2	AAW71376	Aaw71376 Human tel
34	3498	59.3	1132	2	AAY00627	Aay00627 Human tel
35	3498	59.3	1132	2	AAY00638	Aay00638 Truncated
36	3498	59.3	1132	2	AAY28401	Aay28401 Human EST
37	3498	59.3	1132	3	AAY96566	Aay96566 hEST2, a
38	3498	59.3	1132	7	ADC47061	Adc47061 Human TER
39	3498	59.3	1132	7	ADE40482	Ade40482 Human tel
40	3498	59.3	1132	9	AEA38666	Aea38666 Human tel
41	3496	59.2	1132	2	AAW56113	Aaw56113 Human tel
42	3486.5	59.1	1199	2	AAW47007	Aaw47007 Glutathio
43	3471	58.8	1166	2	AAY00647	Aay00647 Telomeras
44	3463	58.7	1405	2	AAW56101	Aaw56101 Enhanced
45	3435	58.2	1120	2	AAY00641	Aay00641 Telomeras

ALIGNMENTS

RESULT 1
AAY26579
ID AAY26579 standard; protein; 1122 AA.
XX
AC AAY26579;
XX
DT 13-SEP-1999 (first entry)
XX
DE Murine telomerase reverse transcriptase (mTERT) enzyme.
XX
KW Telomerase reverse transcriptase; TERT; mouse; telomere length assay;
KW immunogen; enzyme; telomerase-mediated DNA replication.
XX
OS Mus sp.
XX
PN WO9927113-A1.
XX
PD 03-JUN-1999.
XX
PF 25-NOV-1998; 98WO-US025211.
XX
PR 26-NOV-1997; 97US-00979742.
PR 16-MAR-1998; 98US-00042460.
XX
PA (GERO-) GERON CORP.
PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
XX
PI Morin GB, Allsopp R, Depinho R, Greenberg R;
XX
DR WPI; 1999-347722/29.
DR N-PSDB; AAX80994.
XX
PT Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and
PT nucleic acids.
XX
PS Claim 8; Fig 2; 135pp; English.
XX
CC The invention relates to a mouse telomerase reverse transcriptase (mTERT)
CC enzyme. Compositions containing mTERT can be used in telomere length
CC assays. Isolated mTERT is useful as an immunogen for the production of
CC monoclonal or polyclonal antibodies. The method is useful for assessing
CC the degree of purification and identification of new mTERT species, such
CC as an mTERT allele, homolog or isoform, or to screen for modulators
CC (antagonists and agonists) of telomerase-mediated DNA replication.
CC Antagonists and agonists of mTERT can be used to modify the activity of
CC other telomerase enzymes such as human TERT (hTERT). The present sequence
CC represents a mTERT enzyme

```
XX
SQ   Sequence 1122 AA;

  Query Match           100.0%;  Score 5901;  DB 2;  Length 1122;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1122;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHW 60

Qy         61 GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR 120

Qy        121 SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA 180

Qy        181 TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS 240

Qy        241 VPSAKKARCYPVPRVEEGPHRQVLPTPSGKSWVPSPARSPEVPTAEKDLSSKGKVSDLSL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VPSAKKARCYPVPRVEEGPHRQVLPTPSGKSWVPSPARSPEVPTAEKDLSSKGKVSDLSL 300

Qy        301 SGSVCCKHKPSSTSLLSPPRQNAFQLRPFIETRHFLYSRGDGQERLNPSFLLSNLQPNLT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SGSVCCKHKPSSTSLLSPPRQNAFQLRPFIETRHFLYSRGDGQERLNPSFLLSNLQPNLT 360

Qy        361 GARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQYVRLLRSHCRF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQYVRLLRSHCRF 420

Qy        421 RTANQQVTDALNTSPPHLMDLLRLHSSPWQVYGFLRACLCKVVSASLWGTRHNERRFFKN 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 RTANQQVTDALNTSPPHLMDLLRLHSSPWQVYGFLRACLCKVVSASLWGTRHNERRFFKN 480

Qy        481 LKKFISLGKYGKLSLQELMWKMKVEDCHWLRSSPGKDRVPAAEHRLRERILATFLFWLMD 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LKKFISLGKYGKLSLQELMWKMKVEDCHWLRSSPGKDRVPAAEHRLRERILATFLFWLMD 540

Qy        541 TYVVQLLRSFFYITESTFQKNRLFFYRKSVWSKLQSIGVRQHLERVRLRELSQEEVRHHQ 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TYVVQLLRSFFYITESTFQKNRLFFYRKSVWSKLQSIGVRQHLERVRLRELSQEEVRHHQ 600

Qy        601 DTWLAMPICRLRFIPKPNGLRPIVNMSYSMGTRALGRRKQAQHFTQRLKTLFSMLNYERT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 DTWLAMPICRLRFIPKPNGLRPIVNMSYSMGTRALGRRKQAQHFTQRLKTLFSMLNYERT 660

Qy        661 KHPHLMGSSVLGMNDIYRTWRAFVLRVRALDQTPRMYFVKADVTGAYDAIPQGKLVEVVA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 KHPHLMGSSVLGMNDIYRTWRAFVLRVRALDQTPRMYFVKADVTGAYDAIPQGKLVEVVA 720

Qy        721 NMIRHSESTYCIRQYAVVRRDSQGQVHKSFRRQVTTLSDLQPYMGQFLKHLQDSDASALR 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 NMIRHSESTYCIRQYAVVRRDSQGQVHKSFRRQVTTLSDLQPYMGQFLKHLQDSDASALR 780

Qy        781 NSVVIEQSISMNESSSSLFDFFLHFLRHSVVKIGDRCYTQCQGIPQGSSLSTLLCSLCFG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 NSVVIEQSISMNESSSSLFDFFLHFLRHSVVKIGDRCYTQCQGIPQGSSLSTLLCSLCFG 840

Qy        841 DMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQAKTFLSTLVHGVPEYGCMINLQKTVVNF 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 DMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQAKTFLSTLVHGVPEYGCMINLQKTVVNF 900

Qy        901 PVEPGTLGGAAPYQLPAHCLFPWCGLLLDTQTLEVFCDYSGYAQTSIKTSLTFQSVFKAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 PVEPGTLGGAAPYQLPAHCLFPWCGLLLDTQTLEVFCDYSGYAQTSIKTSLTFQSVFKAG 960

Qy        961 KTMRNKLLSVLRLKCHGLFLDLQVNSLQTVCINIYKIFLLQAYRFHACVIQLPFDQRVRK 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 KTMRNKLLSVLRLKCHGLFLDLQVNSLQTVCINIYKIFLLQAYRFHACVIQLPFDQRVRK 1020

Qy       1021 NLTFFLGIISSQASCCYAILKVKNPGMTLKASGSFPPEAAHWLCYQAFLLKLAAHSVIYK 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 NLTFFLGIISSQASCCYAILKVKNPGMTLKASGSFPPEAAHWLCYQAFLLKLAAHSVIYK 1080

Qy       1081 CLLGPLRTAQKLLCRKLPEATMTILKAAADPALSTDFQTILD 1122
              |||||||||||||||||||||||||||||||||||||||||||
Db       1081 CLLGPLRTAQKLLCRKLPEATMTILKAAADPALSTDFQTILD 1122


RESULT 2
ADG90601
ID   ADG90601 standard; protein; 1122 AA.
XX
AC   ADG90601;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Murine TERT SEQ ID NO:4.
XX
KW   mouse; immune response; telomerase reverse transcriptase; TERT;
KW   cytostatic; immunostimulant; cancer; cytotoxic T cell response.
XX
OS   Mus sp.
XX
PN   WO2004002408-A2.
XX
PD   08-JAN-2004.
XX
PF   24-JUN-2003; 2003WO-US019844.
XX
PR   27-JUN-2002; 2002US-0393295P.
XX
PA   (GERO-) GERON CORP.
XX
PI   Majumdar A,  Ferber IA,  Frolkis M,  Wang Z;
XX
DR   WPI; 2004-071946/07.
DR   N-PSDB; ADG90600.
XX
PT   Eliciting an immune response in a mammal specific for its own telomerase
PT   reverse transcriptase (TERT), useful for treating or preventing cancer,
PT   comprises administering a composition containing TERT of another
PT   mammalian species.
XX
PS   Claim 10; SEQ ID NO 4; 44pp; English.
XX
CC   The invention relates to a novel method for eliciting an immune response
CC   in a mammalian subject that is specific for its own telomerase reverse
CC   transcriptase (TERT), comprising administering an immunogenic composition
CC   containing a protein with at least 20 consecutive amino acids of TERT of
CC   another mammalian species, or a nucleic acid encoding the protein. A
CC   composition of the invention has cytostatic, and immunostimulant
CC   activity. The protein or the nucleic acid encoding the protein is useful
CC   in the manufacture of a medicament for the treatment of cancer in a human
CC   or for eliciting a cytotoxic T cell response in a human.
XX
SQ   Sequence 1122 AA;

  Query Match           100.0%;  Score 5901;  DB 8;  Length 1122;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1122;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHW 60

Qy         61 GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR 120

Qy        121 SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA 180
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA 180

Qy         181 TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS 240

Qy         241 VPSAKKARCYPVPRVEEGPHRQVLPTPSGKSWVPSPARSPEVPTAEKDLSSKGKVSDLSL 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 VPSAKKARCYPVPRVEEGPHRQVLPTPSGKSWVPSPARSPEVPTAEKDLSSKGKVSDLSL 300

Qy         301 SGSVCCKHKPSSTSLLSPPRQNAFQLRPFIETRHFLYSRGDGQERLNPSFLLSNLQPNLT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 SGSVCCKHKPSSTSLLSPPRQNAFQLRPFIETRHFLYSRGDGQERLNPSFLLSNLQPNLT 360

Qy         361 GARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQYVRLLRSHCRF 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQYVRLLRSHCRF 420

Qy         421 RTANQQVTDALNTSPPHLMDLLRLHSSPWQVYGFLRACLCKVVSASLWGTRHNERRFFKN 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 RTANQQVTDALNTSPPHLMDLLRLHSSPWQVYGFLRACLCKVVSASLWGTRHNERRFFKN 480

Qy         481 LKKFISLGKYGKLSLQELMWKMKVEDCHWLRSSPGKDRVPAAEHRLRERILATFLFWLMD 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 LKKFISLGKYGKLSLQELMWKMKVEDCHWLRSSPGKDRVPAAEHRLRERILATFLFWLMD 540

Qy         541 TYVVQLLRSFFYITESTFQKNRLFFYRKSVWSKLQSIGVRQHLERVRLRELSQEEVRHHQ 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 TYVVQLLRSFFYITESTFQKNRLFFYRKSVWSKLQSIGVRQHLERVRLRELSQEEVRHHQ 600

Qy         601 DTWLAMPICRLRFIPKPNGLRPIVNMSYSMGTRALGRRKQAQHFTQRLKTLFSMLNYERT 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 DTWLAMPICRLRFIPKPNGLRPIVNMSYSMGTRALGRRKQAQHFTQRLKTLFSMLNYERT 660

Qy         661 KHPHLMGSSVLGMNDIYRTWRAFVLRVRALDQTPRMYFVKADVTGAYDAIPQGKLVEVVA 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 KHPHLMGSSVLGMNDIYRTWRAFVLRVRALDQTPRMYFVKADVTGAYDAIPQGKLVEVVA 720

Qy         721 NMIRHSESTYCIRQYAVVRRDSQGQVHKSFRRQVTTLSDLQPYMGQFLKHLQDSDASALR 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 NMIRHSESTYCIRQYAVVRRDSQGQVHKSFRRQVTTLSDLQPYMGQFLKHLQDSDASALR 780

Qy         781 NSVVIEQSISMNESSSSLFDFFLHFLRHSVVKIGDRCYTQCQGIPQGSSLSTLLCSLCFG 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 NSVVIEQSISMNESSSSLFDFFLHFLRHSVVKIGDRCYTQCQGIPQGSSLSTLLCSLCFG 840

Qy         841 DMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQAKTFLSTLVHGVPEYGCMINLQKTVVNF 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 DMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQAKTFLSTLVHGVPEYGCMINLQKTVVNF 900

Qy         901 PVEPGTLGGAAPYQLPAHCLFPWCGLLLDTQTLEVFCDYSGYAQTSIKTSLTFQSVFKAG 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 PVEPGTLGGAAPYQLPAHCLFPWCGLLLDTQTLEVFCDYSGYAQTSIKTSLTFQSVFKAG 960

Qy         961 KTMRNKLLSVLRLKCHGLFLDLQVNSLQTVCINIYKIFLLQAYRFHACVIQLPFDQRVRK 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 KTMRNKLLSVLRLKCHGLFLDLQVNSLQTVCINIYKIFLLQAYRFHACVIQLPFDQRVRK 1020

Qy        1021 NLTFFLGIISSQASCCYAILKVKNPGMTLKASGSFPPEAAHWLCYQAFLLKLAAHSVIYK 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 NLTFFLGIISSQASCCYAILKVKNPGMTLKASGSFPPEAAHWLCYQAFLLKLAAHSVIYK 1080

Qy        1081 CLLGPLRTAQKLLCRKLPEATMTILKAAADPALSTDFQTILD 1122
               ||||||||||||||||||||||||||||||||||||||||||
Db        1081 CLLGPLRTAQKLLCRKLPEATMTILKAAADPALSTDFQTILD 1122
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RESULT 3
ABB06711
ID   ABB06711 standard; protein; 1122 AA.
XX
AC   ABB06711;
XX
DT   11-JUN-2002  (first entry)
XX
DE   Mouse telomerase protein sequence.
XX
KW   Mouse; telomerase; promoter; telomerase catalyst subunit; TERT; mTERT;
KW   enzyme; transgenic mouse; drug development; anticancer.
XX
OS   Mus sp.
XX
PN   JP2002000121-A.
XX
PD   08-JAN-2002.
XX
PF   23-JUN-2000; 2000JP-00190137.
XX
PR   23-JUN-2000; 2000JP-00190137.
XX
PA   (RIKO-) ZH RIKOGAKU SHINKOKAI.
PA   (KIRI ) KIRIN BREWERY KK.
XX
DR   WPI; 2002-298279/34.
XX
PT   A transgenic mouse comprising a DNA promoter region of mouse telomerase
PT   catalyst subunit (TERT) is used for the development of drugs and
PT   anticancer agents for regeneration of tissues and organs.
XX
PS   Disclosure; Fig 3; 13pp; Japanese.
XX
CC   The present invention describes a transgenic mouse (I) comprising a DNA
CC   construct having a DNA containing a promoter region of mouse telomerase
CC   catalyst subunit (TERT) and a DNA containing a reporter gene connected
CC   under the control of the promoter region. The transgenic mouse can be
CC   used in the development of drugs and anticancer agents for regeneration
CC   of tissues and organs. The present sequence represents the mouse
CC   telomerase protein, which is given in the exemplification of the present
CC   invention
XX
SQ   Sequence 1122 AA;

  Query Match             99.2%;  Score 5854;  DB 5;  Length 1122;
  Best Local Similarity   99.4%;  Pred. No. 0;
  Matches 1115;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy           1 MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHW 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHW 60

Qy          61 GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR 120

Qy         121 SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA 180

Qy         181 TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS 240

Qy         241 VPSAKKARCYPVPRVEEGPHRQVLPTPSGKSWVPSPARSPEVPTAEKDLSSKGKVSDLSL 300
               |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db         241 VPSAKKARCYPVPRVEEGPHRQVLPTFSGKSWVPSPARSPEVPTAEKDLSSKGKVSDLSL 300

Qy         301 SGSVCCKHKPSSTSLLSPPRQNAFQLRPFIETRHFLYSRGDGQERLNPSFLLSNLQPNLT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 SGSVCCKHKPSSTSLLSPPRQNAFQLRPFIETRHFLYSRGDGQERLNPSFLLSNLQPNLT 360

Qy         361 GARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQYVRLLRSHCRF 420
               |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db         361 GARRLVEIIFLGSRPRTSGPLCRTHRLSHRYWQMRPLFQQLLVNHAECQYVRLLRSHCRF 420

Qy         421 RTANQQVTDALNTSPPHLMDLLRLHSSPWQVYGFLRACLCKVVSASLWGTRHNERRFFKN 480
```

```
Db        421 RTANQQVTDALNTSPPHLMDLLRLHSSPWQVYGFLRACLCKVVSASLWGTRHNEHRFFKN 480

Qy        481 LKKFISLGKYGKLSLQELMWKMKVEDCHWLRSSPGKDRVPAAEHRLRERILATFLFWLMD 540

Db        481 LKKFISLGKYGKLSLQELMWKMKVEDCHWLRSSPGKDRVPAAEHRLRERILATFLFWLMD 540

Qy        541 TYVVQLLRSFFYITESTFQKNRLFFYRKSVWSKLQSIGVRQHLERVRLRELSQEEVRHHQ 600

Db        541 TYVVQLLRSPFYITESTFQKNRLFFYRKSVWSKLQSIGVRQHLERVRLRSLSQEEVRHHQ 600

Qy        601 DTWLAMPICRLRFIPKPNGLRPIVNMSYSMGTRALGRRKQAQHFTQRLKTLFSMLNYERT 660

Db        601 DTWLAMPICRLRFIPKPNGLRPIVNMSYSMGTRALGRRKQAQHFTQRLKTLFSMLNYERT 660

Qy        661 KHPHLMGSSVLGMNDIYRTWRAFVLRVRALDQTPRMYFVKADVTGAYDAIPQGKLVEVVA 720

Db        661 KHPHLMGSSVLGMNDIYRTWRAFVLRVRALDQTPRMYFVKADVTGAYDAIPQGKLVEVVA 720

Qy        721 NMIRHSESTYCIRQYAVVRRDSQGQVHKSFRRQVTTLSDLQPYMGQFLKHLQDSDASALR 780

Db        721 NMIRHSESTYCIRQYAVVRRDSQGQVHKSFRRQVTTLSDLQPYMGQFLKHLQDSDASALR 780

Qy        781 NSVVIEQSISMNESSSSLFDFFLHFLRHSVVKIGDRCYTQCQGIPQGSSLSTLLCSLCFG 840

Db        781 NSVVIEQSISMNESSSSLFDFFLHFLRHSVVKIGDRCYTQCQGIPQGSSLSTLLCSLCFG 840

Qy        841 DMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQAKTFLSTLVHGVPEYGCMINLQKTVVNF 900

Db        841 DMENKLFAKVQRDGLLLRFVDDFLLVTPHLDQAKTFLSTLVHGVPEYGCMINLQKTVVNF 900

Qy        901 PVEPGTLGGAAPYQLPAHCLFPWCGLLLDTQTLEVFCDYSGYAQTSIKTSLTFQSVFKAG 960

Db        901 PVEPGTLGGAAPYQLPAHCLFPWCGLLLDTQTLEVFCDYSGYAQTSIKTSLTFQSVFKAG 960

Qy        961 KTMRNKLLSVLRLKCHGLFLDLQVNSLQTVCINIYKIFLLQAYRFHACVIQLPFDQRVRK 1020

Db        961 KTMRNKLLSVLRLKCHGLFLDLQVNSLQTVCINIYKIFLLQAYRFHACVIQLPFDQRVRK 1020

Qy       1021 NLTFFLGIISSQASCCYAILKVKNPGMTLKASGSFPPEAAHWLCYQAFLLKLAAHSVIYK 1080

Db       1021 NLTFFLGIISSQASCCYAILKVKNPGNTLKASGSFPPEAAHWLCYQAFLLKLAAHSVIYK 1080

Qy       1081 CLLGPLRTAQKLLCRKLPEATMTILKAAADPALSTDFQTILD 1122

Db       1081 CLLGPLRTAQKLLCRKLPEATMTILKAAADPALSTDFQTILD 1122
```

RESULT 4
ADG90609
ID ADG90609 standard; protein; 1152 AA.
XX
AC ADG90609;
XX
DT 25-MAR-2004 (first entry)
XX
DE TERT consensus sequence SEQ ID NO:12.
XX
KW immune response; telomerase reverse transcriptase; TERT; cytostatic;
KW immunostimulant; cancer; cytotoxic T cell response.
XX
OS Unidentified.
XX
PN WO2004002408-A2.
XX
PD 08-JAN-2004.
XX
PF 24-JUN-2003; 2003WO-US019844.
XX
PR 27-JUN-2002; 2002US-0393295P.
XX
PA (GERO-) GERON CORP.
XX
PI Majumdar A, Ferber IA, Frolkis M, Wang Z;
XX
DR WPI; 2004-071946/07.
XX
PT Eliciting an immune response in a mammal specific for its own telomerase
PT reverse transcriptase (TERT), useful for treating or preventing cancer,
PT comprises administering a composition containing TERT of another
PT mammalian species.
XX
PS Claim 10; SEQ ID NO 12; 44pp; English.
XX
CC The invention relates to a novel method for eliciting an immune response
CC in a mammalian subject that is specific for its own telomerase reverse
CC transcriptase (TERT), comprising administering an immunogenic composition
CC containing a protein with at least 20 consecutive amino acids of TERT of
CC another mammalian species, or a nucleic acid encoding the protein. A
CC composition of the invention has cytostatic, and immunostimulant
CC activity. The protein or the nucleic acid encoding the protein is useful
CC in the manufacture of a medicament for the treatment of cancer in a human
CC or for eliciting a cytotoxic T cell response in a human.
XX
SQ Sequence 1152 AA;

Query Match 82.3%; Score 4859; DB 8; Length 1152;
Best Local Similarity 83.2%; Pred. No. 0;
Matches 959; Conservative 40; Mismatches 122; Indels 32; Gaps 7;

```
Qy          1 MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHW 60

Db          1 MPRAPRCRAVRALLRSHYREVLPLATFVRRLGPEGRRLVQPGDPAAFRALVAQCLVCVPW 60

Qy         61 GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR 120

Db         61 GARPPPAAPSFHQVSSLKELVARVVQRLCERGERNVLAFGFALLDGARGGPPMAFTTSVR 120

Qy        121 SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA 180

Db        121 SYLPNTVTETLRGSGAWGLLLRRVGDDLLVHLLARCALYLLVAPSCAYQVCGPPLYQIGA 180

Qy        181 TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS 240

Db        181 TTQARPPPHASGRPRRPVGRNFTNLGFCERAWNHSVREAGVPLGLPSPGAKRRGGSASRS 240

Qy        241 VPSAKKARCYPVPRVEEGPHRQVLPTPSGKSWVPSPARSPEVP---TAEKDLSSKGKVSD 297

Db        241 LPLPKKARRGAAPEPERTPVGQGSWTPSGRTRVPSDAGSPVVSPARPAEEDLSSKGKVSD 300

Qy        298 LSLSGSVCCKHKPSS-TSLLSPPRQNAFQLRP-FIETRHFLYSRGDGQERLNPSFLLSNL 355

Db        301 LSLSGSVCCKHKPSSPPSLSSPPRPNAFQLRPVYAETKHFLYSSG-GRERLRPSFLLSNL 359

Qy        356 QPNLTGARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQYVRLLR 415

Db        360 QPSLTGARRLVETIFLGSRPWTSGPLCRTHRLSRRYWQMRPLFQELLGNHARCPYVRLLR 419

Qy        416 SHCRFRTANQQVTDALNTSPP--------------------HLMDLLRLHSSPWQVYGFL 455

Db        420 SHCPLRAAATPVAGALNTSPPQGSVAAPEEVAAPQEQTDSTRLMQLLRQHSSPWQVYGFL 479

Qy        456 RACLCKVVSASLWGTRHNERRFFKNLKKFISLGKYGKLSLQELMWKMKVEDCHWLRSSPG 515

Db        480 RACLCKLVPPGLWGSRHNERRFLKNVKKFISLGKHAKLSLQELTWKMKVRDCAWLRSSPG 539

Qy        516 KDRVPAAEHRLRERILA---TFLFWLMDTYVVQLLRSFFYITESTFQKNRLFFYRKSVWS 572

Db        540 YESVPAAEHRLRERILAKEHPFLFWLMSVYVVELLRSPFYITESTFQKNRLFFYRKSVWS 599

Qy        573 KLQSIGVRQHLERVRLRELSQEEVRHHQDTWLAMPICRLRFIPKPNGLRPIVNMSYSMGT 632

Db        600 KLQSIGVRQHLERVRLRELSQEEVRQHQEAWPAMPICRLRFIPKPNGLRPIVNMSYSMGT 659

Qy        633 RALGRRKQAQHFTQRLKTLFSMLNYERTKHPHLMGSSVLGMNDIYRTWRAFVLRVRALDQ 692
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Db        660 RAFGRRKQAQHFTQRLKTLFSVLNYERTKHPHLLGASVLGMNDIYRTWRTFVLRVRALDP 719

Qy        693 TPRMYFVKADVTGAYDAIPQGKLVEVVANMIRHSESTYCIRQYAVVRRDSQGQVHKSFRR 752

Db        720 TPRMYFVKADVTGAYDAIPQDKLVEVIANMIRHSESTYCIRQYAVVQRDAQGQVHKSFRR 779

Qy        753 QVTTLSDLQPYMGQFLKHLQDSDASALRNSVVIEQSISMNESSSSLFDPFLHFLRHSVVK 812

Db        780 QVSTLSDLQPYMGQFLKHLQDSDASALRNSVVIEQSISLNEASSSLFDPFLRFLRHSVVK 839

Qy        813 IGDRCYTQCQGIPQGSSLSTLLCSLCFGDMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQ 872

Db        840 IGGRCYVQCQGIPQGSSLSTLLCSLCFGDMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQ 899

Qy        873 AKTFLSTLVHGVPEYGCMINLQKTVVNFPVEPGTLGGAAPYQLPAHCLFPWCGLLLDTQT 932

Db        900 AKTFLSTLVRGVPEYGCMINLQKTVVNFPVEPGTLGGTAPYQLPAHCLFPWCGLLLDTQT 959

Qy        933 LEVFCDYSGYAQTSIKTSLTFQSVFKAGKTMRNKLLSVLRLKCHGLFLDLQVNSLQTVCI 992

Db        960 LEVFCDYSGYARTSIKASLTFQRVFKAGKNMRNKLLSVLRLKCHSLFLDLQVNSLQTVCI 1019

Qy        993 NIYKIFLLQAYRFHACVIQLPFDQRVRKNLTFFLGIISSQASCCYAILKVKNPGMTLK-- 1050

Db       1020 NIYKIFLLQAYRFHACVIQLPFDQRVRKNPTFFLGIISSQASCCYAILKVKNAGMTLKAK 1079

Qy       1051 -ASGSFPPEAAHWLCYQAFLLKLAAHSVIYKCLLGPLRTAQKLLCRKLPEATMTILKAAA 1109

Db       1080 GAAGSFPPEAAHWLCYQAFLLKLAAHSVTYKCLLGPLRTAQKQLCRKLPEATMTILEAAA 1139

Qy       1110 DPALSTDFQTILD 1122

Db       1140 DPALSTDFQTILD 1152
```

RESULT 5
ADD21416
ID ADD21416 standard; protein; 1128 AA.
XX
AC ADD21416;
XX
DT 15-JAN-2004 (first entry)
XX
DE Golden hamster TERT protein related to continual cell growth.
XX
KW continual growth; cultured cell; cyclin dependent kinase; cdk4; cdk2;
KW cdk6; activating mutation; cell growth; cell division; cell cycle;
KW cancer-causing agent; continual growth-induced cell; enzyme; TERT;
KW telomerase; Golden hamster.
XX
OS Mesocricetus auratus.
XX
PN WO2003044169-A2.
XX
PD 30-MAY-2003.
XX
PF 15-NOV-2002; 2002WO-US036729.
XX
PR 15-NOV-2001; 2001US-0334760P.
XX
PA (UTEM) UNIV TEMPLE.
XX
PI Reddy PE, Rane SG, Mettus RV;
XX
DR WPI; 2003-449813/42.
XX
PT A composition for reversibly inducing continual growth in normal cells
PT comprises a cyclin dependent kinase protein (e.g. cdk4, cdk2 or cdk6) or
PT its active fragment, derivative, homolog or analog, having an activating
PT mutation.
XX
PS Disclosure; Page 119-121; 77pp; English.
XX

CC This invention relates to a novel composition for inducing a reversible
CC state of a continual growth in cultured cells and comprises at least one
CC compound comprising a cyclin dependent kinase (cdk)4, cdk2 or cdk6
CC protein having an activating mutation. Growth and division of living
CC cells involve a regular series of events and processes that comprise the
CC cell cycle. Cyclin dependent kinases cdk2, cdk4 and cdk6 are involved in
CC the control of G1, the point at which cells irrevocably commit to DNA
CC synthesis and thus enter the cell cycle. The invention is useful in
CC reversibly inducing continual growth in normal cells and may allow the
CC screening of cancer-causing agents with the continual growth-induced
CC cells. The present sequence is that of the golden hamster TERT protein,
CC the catalytic subunit of telomerase, related to the invention. Note: Due
CC to an error in the specification or sequence listing, the Seq ID numbers
CC given in the disclosure do not correspond to those given in the sequence
CC listing. It is therefore unclear which Seq ID number corresponds to which
CC sequence and exactly which sequence is being claimed.
XX
SQ Sequence 1128 AA;

Query Match 80.5%; Score 4751; DB 7; Length 1128;
Best Local Similarity 80.1%; Pred. No. 0;
Matches 904; Conservative 90; Mismatches 127; Indels 8; Gaps 4;

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Qy          1 MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHW 60

Db          1 MPRAPRCRAVRALLRSQYRQVWPLATFVRRLGPEGRQLVQPGDPKVFRTLVARCLVCVPW 60

Qy         61 GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAPGFELLNEARGGPPMAFTSSVR 120

Db         61 DSQPPPADLSFHQVSSLKELVARVVQRLCERGERNVLTFGFALLNGAQGGPPMTFTTSVR 120

Qy        121 SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA 180

Db        121 SYLPNSVTESLRVSGAWMLLLNRVGDDLLVYLLARCALYLLVPPSCAYQVCGSPLYQICA 180

Qy        181 TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS 240

Db        181 TAETWPSVSRIYRPTRPVGRNFTHLGSTHRVRNSSHQEAWKPPPLPSREAKRSLSITNRS 240

Qy        241 VPSAKKARCYPVPRVEEGPHRQVLPTPSGKSWVPSPARSPEVP---TAEKDLSSKGKVSD 297

Db        241 VPPSKKARCDLAPRLEKGPYRQAVPTPSDKTWVPNPAKSHAVPISRTTKEDLSSGVKAPG 300

Qy        298 LSLSGSVCCKHKPSSTSLLSPPRQNAFQLRPFIETRHFLYSRGDGQERLNPSFLLSNLQP 357

Db        301 LSRSGSVCYKHKPSSTSLQSPLCQNAFQLRPYTETKRFLYSREGGRERLNPSFLLNNLQP 360

Qy        358 NLTGARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQYVRLLRSH 417

Db        361 SLTGARRLVEILFLGMRPRTSGPLCGRRRLSKRYWQMRPLFQQLLVNHARCPYVRLLRSH 420

Qy        418 CRFRTANQQVTDALN-TSPPHLMDLLRLHSSPWQVYGFLRACLCKVVSASLWGTRHNERR 476

Db        421 CRFRTAAHQVAGALNTTSPQRLMNLLRLHSSPWQVYGFLQACVGKLVPPGLWGSRHNQRR 480

Qy        477 FFKNLKKFISLGKYGKLSLQELMWKMKVEDCHWLRSSPGKDRVPAAEHRLRERILATFLF 536

Db        481 FFKNVKRFISLGKYDKLSLQELTWKMKVQDCRWLRSSPGNNCVPAAEHRTRERILAVFLF 540

Qy        537 WLMDTYVVQLLRSFFYITESTFQKNRLFFYRKSVWSKLQSIGVRQHLERVRLRELSQEEV 596

Db        541 WLMDAYVVELLRSFFYVTETTFQKNRLFFYRKSMWRRLQSIGVRHHLERVRLQELSQEEV 600

Qy        597 RHHQDTWLAMPICRLRFIPKPNGLRPIVNMSYSMGTRALGRRKQAQHFTQRLKTLFSMLN 656

Db        601 RQRQEAWPAMPICRLRFIPKPSGLRPIVNMSY-MGTRAFDKGKQAQHFTQCLKTLFSVLN 659

Qy        657 YERTKHPHLMGSSVLGMNDIYRTWRAFVLRVRALDQTPRMYFVKADVTGAYDAIPQGKLV 716

Db        660 YELTKHTNLLGASVLGLNDIYRTWRTFVLRVRTLDPAPRMYFVKADVTGAYDAIPQDKLV 719

Qy        717 EVVANMIRHSESTYCIRQYAVVRRDSQGQVHKSFRRQVTTLSDLQPYMGQFLKHLQDSDA 776
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```
Db        720 EVIANMIRHPDNSYCIHQYAVVQRDRQGQIHKSFRRQVSTLSDLQPHMGQFLKHLQDSDT 779

Qy        777 SALRNSVVIEQSISMNESSSSLFDFFLHFLRHSVVKIGDRCYTQCQGIPQGSSLSTLLCS 836

Db        780 SALRNSVVIEQSLSLNEASSSLFDFFLRFVRNSVVKIGGRCYVQCQGIPQGSSLSTLLCS 839

Qy        837 LCFGDMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQAKTFLSTLVHGVPEYGCMINLQKT 896

Db        840 LCFGDMENKLFAEVQQDGLLLRFVDDFLLVTPHLVQAEAFLRALVRGIPEYGCMINLQKT 899

Qy        897 VVNFPVEPGTLGGAAPYQLPAHCLFPWCGLLLDTQTLEVFCDYSGYAQTSIKTSLTFQSV 956

Db        900 VVNFPVDAGTLDGTAPHQLPAHCLFPWCGLLLDTQTLEVLCDYTGYARTSIKASLTFQRT 959

Qy        957 FKAGKTMRNKLLSVLRLKCHGLFLDLQVNSLQTVCINIYKIFLLQAYRFHACVIQLPFDQ 1016

Db        960 FKAGRNMRQKLLAVLRLKCHSLFLDLQMNSLQTVCINVYKIFLLQAYRFHACALQLPFDQ 1019

Qy       1017 RVRKNLTFFLGIISSQASCCYAILKVKNPGMTLK---ASGSFPPEAAHWLCYQAFLLKLA 1073

Db       1020 HVRKNPAFFLSIISNIASCCYSILKVKNAGMTLKAKGASGSFPPEAARWLCYQAFLLKLA 1079

Qy       1074 AHSVIYKCLLGPLRTAQKLLCRKLPEATMTILKAAADPALSTDFQTILD 1122

Db       1080 GHSVTYKCLLGPLRTAQKQLCRKLPRATMAILETAADPALSTDFQTILD 1128


RESULT 6
ADG90603
ID   ADG90603 standard; protein; 1128 AA.
XX
AC   ADG90603;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Hamster TERT SEQ ID NO:6.
XX
KW   hamster; immune response; telomerase reverse transcriptase; TERT;
KW   cytostatic; immunostimulant; cancer; cytotoxic T cell response.
XX
OS   Mesocricetus auratus.
XX
PN   WO2004002408-A2.
XX
PD   08-JAN-2004.
XX
PF   24-JUN-2003; 2003WO-US019844.
XX
PR   27-JUN-2002; 2002US-0393295P.
XX
PA   (GERO-) GERON CORP.
XX
PI   Majumdar A,  Ferber IA,  Frolkis M,  Wang Z;
XX
DR   WPI; 2004-071946/07.
DR   N-PSDB; ADG90602.
XX
PT   Eliciting an immune response in a mammal specific for its own telomerase
PT   reverse transcriptase (TERT), useful for treating or preventing cancer,
PT   comprises administering a composition containing TERT of another
PT   mammalian species.
XX
PS   Claim 10; SEQ ID NO 6; 44pp; English.
XX
CC   The invention relates to a novel method for eliciting an immune response
CC   in a mammalian subject that is specific for its own telomerase reverse
CC   transcriptase (TERT), comprising administering an immunogenic composition
CC   containing a protein with at least 20 consecutive amino acids of TERT of
CC   another mammalian species, or a nucleic acid encoding the protein. A
CC   composition of the invention has cytostatic, and immunostimulant
CC   activity. The protein or the nucleic acid encoding the protein is useful
CC   in the manufacture of a medicament for the treatment of cancer in a human
CC   or for eliciting a cytotoxic T cell response in a human.
XX
SQ   Sequence 1128 AA;

  Query Match            80.5%;  Score 4751;  DB 8;  Length 1128;
  Best Local Similarity  80.1%;  Pred. No. 0;
  Matches  904;  Conservative   90;  Mismatches  127;  Indels    8;  Gaps    4;

Qy          1 MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHW 60

Db          1 MPRAPRCRAVRALLRSQYRQVWPLATFVRRLGPEGRQLVQPGDPKVFRTLVARCLVCVPW 60

Qy         61 GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR 120

Db         61 DSQPPPADLSFHQVSSLKELVARVVQRLCERGERNVLTFGFALLNGAQGGPPMTFTTSVR 120

Qy        121 SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA 180

Db        121 SYLPNSVTESLRVSGAWMLLLNRVGDDLLVYLLARCALYLLVPPSCAYQVCGSPLYQICA 180

Qy        181 TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS 240

Db        181 TAETWPSVSRIYRPTRPVGRNFTHLGSTHRVRNSSHQEAWKPPPLPSREAKRSLSITNRS 240

Qy        241 VPSAKKARCYPVPRVEEGPHRQVLPTPSGKSWVPSPARSPEVP---TAEKDLSSKGKVSD 297

Db        241 VPPSKKARCDLAPRLEKGPYRQAVPTPSDKTWVPNPAKSHAVPISRTTKEDLSSGVKAPG 300

Qy        298 LSLSGSVCCKHKPSSTSLLSPPRQNAFQLRPFIETRHFLYSRGDGQERLNPSFLLSNLQP 357

Db        301 LSRSGSVCYKHKPSSTSLQSPLCQNAFQLRPYTETKRFLYSREGGRERLNPSFLLNNLQP 360

Qy        358 NLTGARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQYVRLLRSH 417

Db        361 SLTGARRLVEILFLGMRPRTSGPLCGRRRLSKRYWQMRPLFQQLLVNHARCPYVRLLRSH 420

Qy        418 CRFRTANQQVTDALN-TSPPHLMDLLRLHSSPWQVYGFLRACLCKVVSASLWGTRHNERR 476

Db        421 CRFRTAAHQVAGALNTTSPQRLMNLLRLHSSPWQVYGFLQACVGKLVPPGLWGSRHNQRR 480

Qy        477 FFKNLKKFISLGKYGKLSLQELMWKMKVEDCHWLRSSPGKDRVPAAEHRLRERILATFLF 536

Db        481 FFKNVKRFISLGKYDKLSLQELTWKMKVQDCRWLRSSPGNNCVPAAEHRTRERILAVFLF 540

Qy        537 WLMDTYVVQLLRSFFYITESTFQKNRLFFYRKSVWSKLQSIGVRQHLERVRLRELSQEEV 596

Db        541 WLMDAYVVELLRSFFYVTETTFQKNRLFFYRKSMWRRLQSIGVRHHLERVRLQELSQEEV 600

Qy        597 RHHQDTWLAMPICRLRFIPKPNGLRPIVNMSYSMGTRALGRRKQAQHFTQRLKTLFSMLN 656

Db        601 RQRQEAWPAMPICRLRFIPKPSGLRPIVNMSY-MGTRAFDKGKQAQHFTQCLKTLFSVLN 659

Qy        657 YERTKHPHLMGSSVLGMNDIYRTWRAFVLRVRALDQTPRMYFVKADVTGAYDAIPQGKLV 716

Db        660 YELTKHTNLLGASVLGLNDIYRTWRTFVLRVRTLDPAPRMYFVKADVTGAYDAIPQDKLV 719

Qy        717 EVVANMIRHSESTYCIRQYAVVRRDSQGQVHKSFRRQVTTLSDLQPYMGQFLKHLQDSDA 776

Db        720 EVIANMIRHPDNSYCIHQYAVVQRDRQGQIHKSFRRQVSTLSDLQPHMGQFLKHLQDSDT 779

Qy        777 SALRNSVVIEQSISMNESSSSLFDFFLHFLRHSVVKIGDRCYTQCQGIPQGSSLSTLLCS 836

Db        780 SALRNSVVIEQSLSLNEASSSLFDFFLRFVRNSVVKIGGRCYVQCQGIPQGSSLSTLLCS 839

Qy        837 LCFGDMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQAKTFLSTLVHGVPEYGCMINLQKT 896

Db        840 LCFGDMENKLFAEVQQDGLLLRFVDDFLLVTPHLVQAEAFLRALVRGIPEYGCMINLQKT 899

Qy        897 VVNFPVEPGTLGGAAPYQLPAHCLFPWCGLLLDTQTLEVFCDYSGYAQTSIKTSLTFQSV 956

Db        900 VVNFPVDAGTLDGTAPHQLPAHCLFPWCGLLLDTQTLEVLCDYTGYARTSIKASLTFQRT 959

Qy        957 FKAGKTMRNKLLSVLRLKCHGLFLDLQVNSLQTVCINIYKIFLLQAYRFHACVIQLPFDQ 1016
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```
Db        960 FKAGRNMRQKLLAVLRLKCHSLFLDLQMNSLQTVCINVYKIFLLQAYRFHACALQLPFDQ 1019

Qy       1017 RVRKNLTFFLGIISSQASCCYAILKVKNPGMTLK---ASGSFPPEAAHWLCYQAFLLKLA 1073
              |||| ||| |||: |||||:|||||| |||||   |||||||||| ||||||||||||
Db       1020 HVRKNPAFFLSIISNIASCCYSILKVKNAGMTLKAKGASGSFPPEAARWLCYQAFLLKLA 1079

Qy       1074 AHSVIYKCLLGPLRTAQKLLCRKLPEATMTILKAAADPALSTDFQTILD 1122
              ||| |||||||||||| |||||| ||| ||: ||||||||||||||
Db       1080 GHSVTYKCLLGPLRTAQKQLCRKLPRATMAILETAADPALSTDFQTILD 1128


RESULT 7
AAW46957
ID   AAW46957 standard; protein; 1132 AA.
XX
AC   AAW46957;
XX
DT   13-AUG-1998  (first entry)
XX
DE   Human telomerase reverse transcriptase.
XX
KW   Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;
KW   cell proliferation; cancer; ageing; ribonucleoprotein.
XX
OS   Homo sapiens.
XX
PN   GB2317891-A.
XX
PD   08-APR-1998.
XX
PF   01-OCT-1997;   97GB-00020890.
XX
PR   01-OCT-1996;   96US-00724643.
PR   18-APR-1997;   97US-00844419.
PR   25-APR-1997;   97US-00846017.
PR   06-MAY-1997;   97US-00851843.
PR   09-MAY-1997;   97US-00854050.
PR   14-AUG-1997;   97US-00911312.
PR   14-AUG-1997;   97US-00912951.
PR   14-AUG-1997;   97US-00915503.
XX
PA   (GERO-) GERON CORP.
PA   (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI   Cech TR,  Lingner J,  Nakamura T,  Chapman KB,  Morin GB,  Harley CB;
PI   Andrews WH;
XX
DR   WPI; 1998-171633/16.
DR   N-PSDB; AAV22379.
XX
PT   Pure and recombinant human Telomerase Reverse Transcriptase and its
PT   variants - are useful in the diagnosis, prognosis and treatment of cell
PT   proliferation conditions especially cancer and ageing.
XX
PS   Claim 3; Fig 17; 387pp; English.
XX
CC   The present sequence represents human telomerase reverse transcriptase
CC   (hTRT), which is a ribonucleoprotein. The present invention also
CC   describes the following methods: (A) determining whether a test compound
CC   is a modulator of hTRT, by detecting the change in hTRT recombinant
CC   protein or polynucleotide, on administration of the compound; (B)
CC   preparation of recombinant telomerase by contacting a protein preparation
CC   of hTRT with a telomerase RNA component; (C) detection of the hTRT RNA or
CC   protein in a sample by binding a relevant probe to the sample and
CC   detecting the complex formed or in the case of RNA detection, amplifying
CC   the product and correlating the presence of complex or amplification
CC   product with presence of hTRT in the sample; and (D) increasing the
CC   proliferation of a vertebrate cell by increasing hTRT expression; and (E)
CC   the use of an agent that causes an increase in cell vertebrate cell
CC   proliferation to create a medicament that inhibits ageing. A protein
CC   preparation of hTRT and the polynucleotide encoding hTRT can be used in
CC   the manufacture of medicaments for inhibiting the effect of ageing or
CC   cancer. Inhibitors of telomerase activity can be used to treat conditions
CC   that are associated with high telomerase activity. A protein preparation
CC   of hTRT can also be used in the new methods
XX
SQ   Sequence 1132 AA;

  Query Match             59.4%;  Score 3505;  DB 2;  Length 1132;
  Best Local Similarity   62.4%;  Pred. No. 0;
  Matches  719;  Conservative  122;  Mismatches  260;  Indels   52;  Gaps   13;

Qy          1 MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHW 60
              | ||||| |||||||| |||| ||||||||||:| |||| ||| :| |||||||: |
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR 120
               ::|||| || ||| ||||||||:|||||| :|||||| ||: |||||| |||:|||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA 180
              ||||||| : || |||| ||| |||||:||:||| |||::|| |||||||||| ||||: |
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS 240
              |   |   ||  | | :|         ::  : | :||  || ||: | :|     | |
Db        181 ATQARPPPHAS-GPRRRLG--------CERAWNHSVREAGVPLGLPAPGARRRGGSASRS 231

Qy        241 VPSAKKARCYPVPRVEEGP-------HRQVLPTPSGKSW-VPSPARSPEVPTAEKDLSSK 292
              :|  |: |     |  |  |       |      || : : | ||||      ||:  | :
Db        232 LPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPAR-----PAEEATSLE 286

Qy        293 GKVSDLSLS-GSVCCKHKPSSTSLLSPPRQNAFQLRP-FIETRHFLYSRGDGQERLNPSF 350
              | :|    |  ||  :|    |   |||       | : ||:||||| || :|:| |||
Db        287 GALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGD-KEQLRPSF 345

Qy        351 LLSNLQPNLTGARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQY 410
              |||:|:|:|||||||| ||||||    |   |  || :|||||||| :|| |||:| |
Db        346 LLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPY 405

Qy        411 VRLLRSHCRFRTANQQVTDAL-----------------NTSPPHLMDLLRLHSSPWQVY 452
                ||::||  | |   || |                    :| |  |: ||| ||||||||
Db        406 GVLLKTHCPLRAA---VTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVY 462

Qy        453 GFLRACLCKVVSASLWGTRHNERRFFKNLKKFISLGKYGKLSLQELMWKMKVEDCHWLRS 512
              ||:|||| ::|   |||:|||||| :| |||||||: ||||||| ||| | || |||
Db        463 GFVRACLRRLVPPGLWGSRHNERRFLRNTKKPISLGKHAKLSLQELTWKMSVRDCAWLRR 522

Qy        513 SPGKDRVPAAEHRLRERILATFLFWLMDTYVVQLLRSFFYITESTFQKNRLFFYRKSVWS 572
              |||   |||||||||| ||| || |||  |||:||||||:||:|||||||||||||||
Db        523 SPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWS 582

Qy        573 KLQSIGVRQHLERVRLRELSQEEVRHHQDTWLAMPICRLRFIPKPNGLRPIVNMSYSMGT 632
              ||||||:||||:||:|||||: ||| |::   |:   |||||||:|||||||| | :|
Db        583 KLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGA 642

Qy        633 RALGRRKQAQHFTQRLKTLFSMLNYERTKHPHLMGSSVLGMNDIYRTWRAFVLRVRALDQ 692
              |   | |:|:  | |:| |||:||||| : | |:|:||||::||:| || ||||||| |
Db        643 RTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDP 702

Qy        693 TPRMYFVKADVTGAYDAIPQGKLVEVVANMIRHSESTYCIRQYAVVRRDSQGQVHKSFRR 752
              | :|||| |||||||| ||| :| ||:|::|:  ::|||:|:||||:: : | | |:|
Db        703 PPELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PQNTYCVRRYAVVQKAAHGHVRKAFKS 761

Qy        753 QVTTLSDLQPYMGQFLKHLQDSDASALRNSVVIEQSISMNESSSSLFDFFLHFLRHSVVK 812
              |:||:|||||| ||: |||::  | ||::|||||| |:||:|| ||| || |: | |:
Db        762 HVSTLTDLQPYMRQFVAHLQET--SPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVR 819

Qy        813 IGDRCYTQCQGIPQGSSLSTLLCSLCFGDMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQ 872
              |  : | |||||||||| |||||||||:|||||||| ::|||||| ||||||||||
Db        820 IRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH 879

Qy        873 AKTFLSTLVHGVPEYGCMINLQKTVVNFPVEPGTLGGAAPYQLPAHCLFPWCGLLLDTQT 932
              ||||| ||| |||||||::||:|||||||||   ||| |  |:||| ||||||||||:|
Db        880 AKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRT 939
```

```
Qy        933 LEVFCDYSGYAQTSIKTSLTFQSVFKAGKTMRNKLLSVLRLKCHGLFLDLQVNSLQTVCI 992
              |||  ||| ||:|||: ||||   ||||: || ||  ||||||| ||||||||||||||
Db        940 LEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT 999

Qy        993 NIYKIFLLQAYRFHACVIQLPFDQRVRKNLTFFLGIISSQASCCYAILKVKNPGMTLKAS 1052
              ||||| ||||||||||:|||| |:| || |||| :||  || ||:||| || ||:| |
Db       1000 NIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAK 1059

Qy       1053 GS---FPPEAAHWLCYQAFLLKLAAHSVIYKCLLGPLRTAQKLLCRKLPEATMTILKAAA 1109
              |:    | ||  |||:|||||||  | | |  ||| |||||  | ||||  |:| |:|||
Db       1060 GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA 1119

Qy       1110 DPALSTDFQTILD 1122
              :||| :||:||||
Db       1120 NPALPSDFKTILD 1132
```

RESULT 8
AAW90251
ID AAW90251 standard; protein; 1132 AA.
XX
AC AAW90251;
XX
DT 24-MAY-1999 (first entry)
XX
DE Human catalytic telomerase sub-unit protein.
XX
KW Human; catalytic telomerase subunit; therapy; diagnosis; hTC; assay;
KW modulator; treatment; inhibit; cellular disorder; death; defect; cancer;
KW ageing; antisense; neoplastic cell; telomerase-related condition;
KW tumour cell.
XX
OS Homo sapiens.
XX
PN WO9859040-A2.
XX
PD 30-DEC-1998.
XX
PF 09-JUN-1998; 98WO-EP003468.
XX
PR 20-JUN-1997; 97DE-01026329.
PR 26-MAR-1998; 98DE-01013274.
PR 14-APR-1998; 98DE-01016496.
XX
PA (FARB) BAYER AG.
XX
PI Hagen G, Siegmund H, Weichel W, Wick M, Zubov D;
XX
DR WPI; 1999-081276/07.
DR N-PSDB; AAV72117.
XX
PT New catalytically active subunit of human telomerase - used in the
PT modulation of telomerase activity, particularly for treating cancer and
PT ageing.
XX
PS Claim 2; Fig 2; 76pp; German.
XX
CC This sequence represents a novel human catalytic telomerase sub-unit
CC (hTC). This protein can be used in screening assays to identify
CC modulators of telomerase and to treat or inhibit cellular disorders,
CC death, defects and/or other pathological processes involving telomerase,
CC particularly cancer and ageing (also suitable for this are agents that
CC stimulate, inhibit or mimic the activity of the subunit). Antisense
CC nucleic acids inhibit telomerase action (by binding to specific mRNA),
CC particularly in neoplastic cells and may be expressed in vivo. Antibodies
CC and fragments of the protein, used as probes or primers, are used to
CC diagnose telomerase-related conditions (especially neoplasia) by (i)
CC detecting abnormal levels of the subunit protein in body fluids or
CC tissues or (ii) by measuring the amount of the encoding nucleic acid.
CC Expression of the nucleic acid encoding the subunit mRNA is confined to
CC tumour cells, in contrast to the ubiquitous expression of the telomerase
CC RNA subunit
XX

SQ Sequence 1132 AA;

Query Match 59.4%; Score 3505; DB 2; Length 1132;
Best Local Similarity 62.4%; Pred. No. 0;
Matches 719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;

```
Qy          1 MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHW 60
              | ||||| |||||||| |||| |||||||||||:| |||| ||| :| |||||||: |
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR 120
               ::|||  || ||| |||||||:|||||  :|||||| ||: |||||| |||:|||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA 180
              ||||||| : || |||| ||| |||||:||:||| |||::|| |||||||| |||| |
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS 240
              |   |   ||  | | :|          ::  : | :||  || ||: | :|     | |
Db        181 ATQARPPPHAS-GPRRRLG--------CERAWNHSVREAGVPLGLPAPGARRRGGSASRS 231

Qy        241 VPSAKKARCYPVPRVEEGP-------HRQVLPTPSGKSW-VPSPARSPEVPTAEKDLSSK 292
              :|  |: |     |  |  |       |      || : : | ||||      ||:  | :
Db        232 LPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPAR-----PAEEATSLE 286

Qy        293 GKVSDLSLS-GSVCCKHKPSSTSLLSPPRQNAFQLRP-FIETRHFLYSRGDGQERLNPSF 350
              | :|    |  ||  :|     |  |||       | : ||:||||| || :|:| |||
Db        287 GALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGD-KEQLRPSF 345

Qy        351 LLSNLQPNLTGARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQY 410
              |||:|:|:|||||||| |||||||    |   || :||||||| :|| |||:| |
Db        346 LLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPY 405

Qy        411 VRLLRSHCRFRTANQQVTDAL-----------------NTSPPHLMDLLRLHSSPWQVY 452
              ||::||  | |   || |                    :| |  |: ||| ||||||||
Db        406 GVLLKTHCPLRAA---VTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVY 462

Qy        453 GFLRACLCKVVSASLWGTRHNERRFFKNLKKFISLGKYGKLSLQELMWKMKVEDCHWLRS 512
              ||:|||| ::|   |||:|||||||| :| ||||||||: ||||||| ||| | || |||
Db        463 GFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRR 522

Qy        513 SPGKDRVPAAEHRLRERILATFLFWLMDTYVVQLLRSFFYITESTFQKNRLFFYRKSVWS 572
              |||   |||||||||| ||| || |||  |||:|||||||:||:|||||||||||||||
Db        523 SPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWS 582

Qy        573 KLQSIGVRQHLERVRLRELSQEEVRHHQDTWLAMPICRLRFIPKPNGLRPIVNMSYSMGT 632
              ||||||:||||:||:|||||: ||| |::   |:   ||||||||:|||||||| | :|
Db        583 KLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGA 642

Qy        633 RALGRRKQAQHFTQRLKTLFSMLNYERTKHPHLMGSSVLGMNDIYRTWRAFVLRVRALDQ 692
              |   | |:|:  | |:| |||:||||| : | |:|:||||::||:| || |||||| |
Db        643 RTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDP 702

Qy        693 TPRMYFVKADVTGAYDAIPQGKLVEVVANMIRHSESTYCIRQYAVVRRDSQGQVHKSFRR 752
              | :|||| ||||||| ||| :| ||:|::|:  ::|||:|:|||||:: : | | |:|:
Db        703 PPELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PQNTYCVRRYAVVQKAAHGHVRKAFKS 761

Qy        753 QVTTLSDLQPYMGQFLKHLQDSDASALRNSVVIEQSISMNESSSSLFDFFLHFLRHSVVK 812
              |:||:|||||| ||: |||::  | ||::|||||| |:||:|| ||| || |: |  |:
Db        762 HVSTLTDLQPYMRQFVAHLQET--SPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVR 819

Qy        813 IGDRCYTQCQGIPQGSSLSTLLCSLCFGDMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQ 872
              |  : | |||||||| |||||||||:|||||||| ::|||||| ||||||||||
Db        820 IRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH 879

Qy        873 AKTFLSTLVHGVPEYGCMINLQKTVVNFPVEPGTLGGAAPYQLPAHCLFPWCGLLLDTQT 932
              ||||| ||| |||||||::||:|||||||||    ||| |  |:||| ||||||||||:|
Db        880 AKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRT 939

Qy        933 LEVFCDYSGYAQTSIKTSLTFQSVFKAGKTMRNKLLSVLRLKCHGLFLDLQVNSLQTVCI 992
              |||  ||| ||:|||: ||||   ||||: || ||  ||||||| ||||||||||||||
Db        940 LEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT 999
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```
Qy        993 NIYKIFLLQAYRFHACVIQLPFDQRVRKNLTFFLGIISSQASCCYAILKVKNPGMTLKAS 1052
              ||||| |||||||||||:|||| |:| || |||| :|| || ||:||| || ||:| |
Db       1000 NIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAK 1059

Qy       1053 GS---FPPEAAHWLCYQAFLLKLAAHSVIYKCLLGPLRTAQKLLCRKLPEATMTILKAAA 1109
              |:    | ||  |||:|||||||  | | |  ||| |||||  | ||||  |:| |:|||
Db       1060 GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA 1119

Qy       1110 DPALSTDFQTILD 1122
              :||| :||:||||
Db       1120 NPALPSDFKTILD 1132


RESULT 9
AAY28881
ID   AAY28881 standard; protein; 1132 AA.
XX
AC   AAY28881;
XX
DT   17-JAN-2000  (first entry)
XX
DE   Human telomerase reverse transcriptase protein.
XX
KW   Human telomerase reverse transcriptase protein; hTRT; telomerase; hEST2;
KW   catalytic protein component; cell proliferative capacity; DNA primer;
KW   telomerase substrate; telomeric DNA synthesis; cell immortality;
KW   neoplastic phenotype; diagnostic application; prognostic application;
KW   telomerase related condition; cancer; therapeutic agent;
KW   telomerase expression; telomerase activity.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 608
FT                   /note= "Corresponds to cac codon"
XX
PN   WO9950279-A1.
XX
PD   07-OCT-1999.
XX
PF   31-MAR-1999;   99WO-US007160.
XX
PR   31-MAR-1998;   98US-00052919.
XX
PA   (GERO-) GERON CORP.
PA   (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI   Cech TR,  Lingner J,  Nakamura T,  Chapman KB,  Morin GB,  Harley CB;
PI   Andrews WH;
XX
DR   WPI; 1999-610834/52.
DR   N-PSDB; AAZ08150.
XX
PT   Antisense polynucleotides for human telomerase reverse transcriptase used
PT   for diagnosing or treating cancer.
XX
PS   Claim 2; Fig 2; 31pp; English.
XX
CC   The present sequence is human telomerase reverse transcriptase protein.
CC   This is the catalytic protein component of telomerase and is also
CC   referred to as hEST2. HTRT has the ability to extend a DNA primer that
CC   functions as a telomerase substrate for telomeric DNA synthesis. This
CC   correlates with cell proliferative capacity, cell immortality, and the
CC   development of a neoplastic phenotype. Human TRT antisense
CC   oligonucleotides are useful for diagnostic or prognostic applications to
CC   telomerase related conditions, including cancer. They are also useful as
CC   therapeutic agents, for inhibition of telomerase expression and activity
XX
SQ   Sequence 1132 AA;

  Query Match             59.4%;  Score 3505;  DB 2;  Length 1132;
  Best Local Similarity   62.4%;  Pred. No. 0;

  Matches  719;  Conservative  122;  Mismatches  260;  Indels   52;  Gaps   13;

Qy          1 MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHW 60
              | ||||| |||||||| |||| |||||||||||:| |||| |||  :| ||||||||: |
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR 120
               ::|||| || ||| ||||||||:|||||| :||||||| ||: |||||| |||:|||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA 180
              ||||||| : || |||| ||| |||||:||:||| |||::|| |||||||||| |||| |
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS 240
              | |  |  || | | :|          ::  :  | :||  || ||: | :|      | |
Db        181 ATQARPPPHAS-GPRRRLG--------CERAWNHSVREAGVPLGLPAPGARRRGGSASRS 231

Qy        241 VPSAKKARCYPVPRVEEGP-------HRQVLPTPSGKSW-VPSPARSPEVPTAEKDLSSK 292
              :|  |: |    |  | |          |      || : : | ||||      ||:  | :
Db        232 LPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPAR-----PAEEATSLE 286

Qy        293 GKVSDLSLS-GSVCCKHKPSSTSLLSPPRQNAFQLRP-FIETRHFLYSRGDGQERLNPSF 350
              | :|    |  ||  :|     |   |||        | : ||:||||| || :|:| |||
Db        287 GALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGD-KEQLRPSF 345

Qy        351 LLSNLQPNLTGARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQY 410
              |||:|:|:|||||||| |||||||   |  |  || :|||||||| :|| |||:| |
Db        346 LLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPY 405

Qy        411 VRLLRSHCRFRTANQQVTDAL-----------------NTSPPHLMDLLRLHSSPWQVY 452
                ||::||  | |  || |                  :| |  |: ||| ||||||||
Db        406 GVLLKTHCPLRAA---VTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVY 462

Qy        453 GFLRACLCKVVSASLWGTRHNERRFFKNLKKFISLGKYGKLSLQELMWKMKVEDCHWLRS 512
              ||:|||| ::|   |||:|||||| :| |||||||: ||||||| ||| | || |||
Db        463 GFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRR 522

Qy        513 SPGKDRVPAAEHRLRERILATFLFWLMDTYVVQLLRSFFYITESTFQKNRLFFYRKSVWS 572
              |||   |||||||||| ||| || |||  |||:|||||||:||:|||||||||||||||
Db        523 SPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWS 582

Qy        573 KLQSIGVRQHLERVRLRELSQEEVRHHQDTWLAMPICRLRFIPKPNGLRPIVNMSYSMGT 632
              ||||||:||||:|||||||: ||| |::   |:   ||||||||:|||||||| | :|
Db        583 KLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGA 642

Qy        633 RALGRRKQAQHFTQRLKTLFSMLNYERTKHPHLMGSSVLGMNDIYRTWRAFVLRVRALDQ 692
              |   | |:|:  | |:| |||:||||| : | |:|:||||::||:| || ||||||| |
Db        643 RTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDP 702

Qy        693 TPRMYFVKADVTGAYDAIPQGKLVEVVANMIRHSESTYCIRQYAVVRRDSQGQVHKSFRR 752
              | :|||| ||||||| ||| :| ||:|::|:  ::|||:|:||||:: : | | |:|:
Db        703 PPELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PQNTYCVRRYAVVQKAAHGHVRKAFKS 761

Qy        753 QVTTLSDLQPYMGQFLKHLQDSDASALRNSVVIEQSISMNESSSSLFDFFLHFLRHSVVK 812
              |:||:|||||| ||: |||::  | ||::|||||| |:||:|| ||| || |: |  |:
Db        762 HVSTLTDLQPYMRQFVAHLQET--SPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVR 819

Qy        813 IGDRCYTQCQGIPQGSSLSTLLCSLCFGDMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQ 872
              |  : | |||||||| |||||||||:|||||||| ::|||||| ||||||||||
Db        820 IRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH 879

Qy        873 AKTFLSTLVHGVPEYGCMINLQKTVVNFPVEPGTLGGAAPYQLPAHCLFPWCGLLLDTQT 932
              ||||| ||| |||||||::||:|||||||||    ||| |  |:||| ||||||||||:|
Db        880 AKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRT 939

Qy        933 LEVFCDYSGYAQTSIKTSLTFQSVFKAGKTMRNKLLSVLRLKCHGLFLDLQVNSLQTVCI 992
              |||  ||| ||:|||: |||    ||||: || ||  |||||| ||||||||||||||||
Db        940 LEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT 999

Qy        993 NIYKIFLLQAYRFHACVIQLPFDQRVRKNLTFFLGIISSQASCCYAILKVKNPGMTLKAS 1052
              ||||| |||||||||||:|||| |:| || |||| :|| || ||:||| || ||:| |
Db       1000 NIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAK 1059
```

```
Qy       1053 GS---FPPEAAHWLCYQAPLLKLAAHSVIYKCLLGPLRTAQKLLCRKLPEATMTILKAAA 1109
              |:    | ||  |||:|||||||  | | |  ||| |||||  | ||||  |:| |:|||
Db       1060 GAAGPLPSEAVQWLCHQAPLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA 1119

Qy       1110 DPALSTDFQTILD 1122
              :||| :||:||||
Db       1120 NPALPSDFKTILD 1132


RESULT 10
AAY32090
ID   AAY32090 standard; protein; 1132 AA.
XX
AC   AAY32090;
XX
DT   17-JAN-2000  (first entry)
XX
DE   Human telomerase reverse transcriptase (hTRT).
XX
KW   Telomerase reverse transcriptase; human; hTRT; cell proliferation;
KW   cancer.
XX
OS   Homo sapiens.
XX
PN   WO9950386-A2.
XX
PD   07-OCT-1999.
XX
PF   31-MAR-1999;   99WO-US007097.
XX
PR   31-MAR-1998;   98US-00052864.
PR   03-AUG-1998;   98US-00128354.
XX
PA   (GERO-) GERON CORP.
XX
PI   Morin GB;
XX
DR   WPI; 1999-610842/52.
DR   N-PSDB; AAZ20279.
XX
PT   New catalytic polypeptide and polynucleotide, useful for increasing
PT   catalytic activity in a cell.
XX
PS   Claim 13; Fig 1; 24pp; English.
XX
CC   The present sequence represents human telomerase reverse transcriptase
CC   (hTRT). Human telomerase is a target for diagnosing and treating diseases
CC   relating to cell proliferation and senescence, such as cancer, or for
CC   increasing the proliferative capacity of a cell. A claimed method for
CC   increasing the proliferative capacity of a vertebrate cell, especially a
CC   human or other mammalian cell, involves introducing into the cell a
CC   recombinant hTRT polynucleotide encoding an hTRT variant in which
CC   residues 192-323, 200-323, 192-271, 200-271, 222-240, 415-450, 192-323
CC   and 415-450, or 192-271 and 415-450 of the present sequence are deleted.
CC   A claimed method of preparing recombinant telomerase involves contacting
CC   a recombinant hTRT deletion mutant (as above) with a telomerase RNA
CC   component such that the 2 proteins associate to form a complex capable of
CC   catalysing the addition of nucleotides to a telomerase substrate. A
CC   claimed method for reducing telomerase activity in a cell involves
CC   introducing a recombinant polynucleotide encoding an hTRT variant having
CC   a deletion of amino acids 192-450, 560-565, 637-660, 638-660, 748-764 or
CC   1055-1071 of the present sequence
XX
SQ   Sequence 1132 AA;

  Query Match             59.4%;  Score 3505;  DB 2;  Length 1132;
  Best Local Similarity   62.4%;  Pred. No. 0;
  Matches  719;  Conservative  122;  Mismatches  260;  Indels   52;  Gaps   13;

Qy          1 MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHW 60
              | ||||| |||||||| |||| |||||||||||:| |||| |||  :| |||||||: |
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR 120
              ::|||| || ||| |||||||:|||||  :|||||| ||: |||||| |||:|||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA 180
              ||||||| : || |||| ||| |||||:||:||| |||::|| ||||||||| ||||: |
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS 240
              |   |  ||  | | :|         ::  : | :||  || ||: | :|     | |
Db        181 ATQARPPPHAS-GPRRRLG--------CERAWNHSVREAGVPLGLPAPGARRRGGSASRS 231

Qy        241 VPSAKKARCYPVPRVEEGP-------HRQVLPTPSGKSW-VPSPARSPEVPTAEKDLSSK 292
              :|  |: |   |  |  |       |     || : : | ||||      ||:  | :
Db        232 LPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPAR-----PAEEATSLE 286

Qy        293 GKVSDLSLS-GSVCCKHKPSSTSLLSPPRQNAFQLRP-FIETRHFLYSRGDGQERLNPSF 350
              | :|    |  ||  :|     |  |||       | : ||:||||| || :|:| |||
Db        287 GALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGD-KEQLRPSF 345

Qy        351 LLSNLQPNLTGARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQY 410
              |||:|:|:|||||||| |||||||   |   | || :|||||||| :|| |||:| |
Db        346 LLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPY 405

Qy        411 VRLLRSHCRFRTANQQVTDAL-----------------NTSPPHLMDLLRLHSSPWQVY 452
              ||::||  | |   || |                   :| |  |: ||| ||||||||
Db        406 GVLLKTHCPLRAA---VTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVY 462

Qy        453 GFLRACLCKVVSASLWGTRHNERRFFKNLKKFISLGKYGKLSLQELMWKMKVEDCHWLRS 512
              ||:|||| ::|   |||:|||||||| :| ||||||||: ||||||| ||| | || |||
Db        463 GFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRR 522

Qy        513 SPGKDRVPAAEHRLRERILATFLFWLMDTYVVQLLRSFFYITESTFQKNRLFFYRKSVWS 572
              |||   |||||||||| ||| || |||  |||:||||||||:||:|||||||||||||
Db        523 SPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWS 582

Qy        573 KLQSIGVRQHLERVRLRELSQEEVRHHQDTWLAMPICRLRFIPKPNGLRPIVNMSYSMGT 632
              ||||||:||||:||:|||||: ||| |::   |:   ||||||||:|||||||| | :|
Db        583 KLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGA 642

Qy        633 RALGRRKQAQHFTQRLKTLFSMLNYERTKHPHLMGSSVLGMNDIYRTWRAFVLRVRALDQ 692
              |   | |:|:  | |:| |||:|||||  : | |:|:||||::||:| || ||||||| |
Db        643 RTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDP 702

Qy        693 TPRMYFVKADVTGAYDAIPQGKLVEVVANMIRHSESTYCIRQYAVVRRDSQGQVHKSFRR 752
              | :|||| ||||||| ||| :| ||:|::|:  ::|||:|:||||:: : | | |:|:
Db        703 PPELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PQNTYCVRRYAVVQKAAHGHVRKAFKS 761

Qy        753 QVTTLSDLQPYMGQFLKHLQDSDASALRNSVVIEQSISMNESSSSSLFDFFLHFLRHSVVK 812
              |:||:|||||| ||: |||::  | ||::|||||| |:||:|| ||| || |: |  |:
Db        762 HVSTLTDLQPYMRQFVAHLQET--SPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVR 819

Qy        813 IGDRCYTQCQGIPQGSSLSTLLCSLCFGDMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQ 872
              |  : | ||||||||| |||||||||:|||||||| ::|||||| ||||||||||
Db        820 IRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH 879

Qy        873 AKTFLSTLVHGVPEYGCMINLQKTVVNFPVEPGTLGGAAPYQLPAHCLFPWCGLLLDTQT 932
              ||||| ||| |||||||::||:|||||||||    ||| |  |:||| ||||||||||:|
Db        880 AKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRT 939

Qy        933 LEVFCDYSGYAQTSIKTSLTFQSVFKAGKTMRNKLLSVLRLKCHGLFLDLQVNSLQTVCI 992
              |||  ||| ||:|||: ||||   ||||: || ||  ||||||| ||||||||||||||
Db        940 LEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT 999

Qy        993 NIYKIFLLQAYRFHACVIQLPFDQRVRKNLTFFLGIISSQASCCYAILKVKNPGMTLKAS 1052
              ||||| |||||||||||:|||| |:| || |||| :||  || ||:||| || ||:| |
Db       1000 NIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAK 1059

Qy       1053 GS---FPPEAAHWLCYQAPLLKLAAHSVIYKCLLGPLRTAQKLLCRKLPEATMTILKAAA 1109
              |:    | ||  |||:|||||||  | | |  ||| |||||  | ||||  |:| |:|||
Db       1060 GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA 1119
```

```
Qy       1110 DPALSTDFQTILD 1122
              :||| :||:||||
Db       1120 NPALPSDFKTILD 1132


RESULT 11
AAY43621
ID   AAY43621 standard; protein; 1132 AA.
XX
AC   AAY43621;
XX
DT   26-JAN-2000  (first entry)
XX
DE   A human telomerase reverse transcriptase (TRT) polypeptide.
XX
KW   Human; telomerase reverse transcriptase; TRT; T lymphocyte activation;
KW   dendritic cell; telomerase activity; cancer cell; proliferating cell;
KW   immunological destruction; telomerase; cancer; proliferation disease.
XX
OS   Homo sapiens.
XX
PN   WO9950392-A1.
XX
PD   07-OCT-1999.
XX
PF   30-MAR-1999;   99WO-US006898.
XX
PR   31-MAR-1998;   98US-0112006P.
XX
PA   (GERO-) GERON CORP.
XX
PI   Gaeta FCA;
XX
DR   WPI; 1999-610845/52.
DR   N-PSDB; AAZ30154.
XX
PT   Eliciting an in vivo immune response for prevention and treatment of
PT   cancers.
XX
PS   Claim 3; Fig 1; 26pp; English.
XX
CC   The present sequence represents a human telomerase reverse transcriptase
CC   (TRT) polypeptide. The protein is used in the method of the invention.
CC   The specification describes a method for activating a T lymphocyte,
CC   comprising contacting the T lymphocyte with a dendritic cell that
CC   expresses a TRT peptide in the context of a MHC class I or MHC class II
CC   molecule. The protein causes induction of an in vivo immunological
CC   response to telomerase activity. Cancer cells are characterized by
CC   expression of endogenous TRT gene and the presence of detectable
CC   telomerase activity. Therefore, by eliciting a specific immune response
CC   to TRT or to TRT-expressing cells, it is possible to selectively target
CC   proliferating cells for immunological destruction. The method is used for
CC   eliciting an in vivo immune response to telomerase by activating a T
CC   lymphocyte, and is useful for prevention and treatment of cancers and
CC   other proliferation diseases/conditions
XX
SQ   Sequence 1132 AA;

  Query Match             59.4%;  Score 3505;  DB 2;  Length 1132;
  Best Local Similarity   62.4%;  Pred. No. 0;
  Matches  719;  Conservative  122;  Mismatches  260;  Indels   52;  Gaps   13;

Qy          1 MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHW 60
              | ||||| |||||||| |||| ||||||||||:| |||| ||| :| ||||||||: |
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR 120
               ::|||  || ||| |||||||||:||||||  :|||||| ||: |||||| |||:|||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA 180
              ||||||| : || |||| ||| |||||:||:||| |||::|| ||||||||| ||||: |
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS 240
              |   |   ||  | | :|         ::  : | :||  || ||: | :|     | |
Db        181 ATQARPPPHAS-GPRRRLG--------CERAWNHSVREAGVPLGLPAPGARRRGGSASRS 231

Qy        241 VPSAKKARCYPVPRVEEGP-------HRQVLPTPSGKSW-VPSPARSPEVPTAEKDLSSK 292
              :|  |: |    |  | |       |      || : : | ||||       ||:  | :
Db        232 LPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPAR-----PAEEATSLE 286

Qy        293 GKVSDLSLS-GSVCCKHKPSSTSLLSPPRQNAFQLRP-FIETRHFLYSRGDGQERLNPSF 350
              | :|    |  ||  :|    |  |||       | : ||:||||| || :|:| |||
Db        287 GALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGD-KEQLRPSF 345

Qy        351 LLSNLQPNLTGARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQY 410
              |||:|:|:|||||||| |||||||    |   || :|||||||| :|| |||:| |
Db        346 LLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPY 405

Qy        411 VRLLRSHCRFRTANQQVTDAL-----------------NTSPPHLMDLLRLHSSPWQVY 452
              ||::||  | |   || |                   :| |  |: ||| ||||||||
Db        406 GVLLKTHCPLRAA---VTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVY 462

Qy        453 GFLRACLCKVVSASLWGTRHNERRFFKNLKKFISLGKYGKLSLQELMWKMKVEDCHWLRS 512
              ||:|||| ::|   |||:|||||| :| |||||||: ||||||| ||| | || |||
Db        463 GFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRR 522

Qy        513 SPGKDRVPAAEHRLRERILATFLFWLMDTYVVQLLRSFFYITESTFQKNRLFFYRKSVWS 572
              |||   |||||||||| ||| || |||  |||:|||||||:||:|||||||||||||||
Db        523 SPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWS 582

Qy        573 KLQSIGVRQHLERVRLRELSQEEVRHHQDTWLAMPICRLRFIPKPNGLRPIVNMSYSMGT 632
              ||||||:||||:||:|||||: ||| |::   |:   ||||||||:|||||||| | :|
Db        583 KLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGA 642

Qy        633 RALGRRKQAQHFTQRLKTLFSMLNYERTKHPHLMGSSVLGMNDIYRTWRAFVLRVRALDQ 692
              |    | :|:  | |:| |||:||||| : | |:|:||||::||:| || |||||||  |
Db        643 RTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDP 702

Qy        693 TPRMYFVKADVTGAYDAIPQGKLVEVVANMIRHSESTYCIRQYAVVRRDSQGQVHKSFRR 752
              | :|||| ||||||| ||| :| ||:|::|:  ::|||:|:||||:: : | | |:|:
Db        703 PPELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PQNTYCVRRYAVVQKAAHGHVRKAFKS 761

Qy        753 QVTTLSDLQPYMGQFLKHLQDSDASALRNSVVIEQSISMNESSSSLFDFFLHFLRHSVVK 812
              |:||:|||||| ||: |||::  | ||::|||||| |:||:|| ||| || |: |  |:
Db        762 HVSTLTDLQPYMRQFVAHLQET--SPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVR 819

Qy        813 IGDRCYTQCQGIPQGSSLSTLLCSLCFGDMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQ 872
              |  : | |||||||||| ||||||||:||||||||| ::|||||| ||||||||||
Db        820 IRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH 879

Qy        873 AKTFLSTLVHGVPEYGCMINLQKTVVNFPVEPGTLGGAAPYQLPAHCLFPWCGLLLDTQT 932
              ||||| ||| |||||||::||:|||||||||    ||| |  |:||| ||||||||||:|
Db        880 AKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRT 939

Qy        933 LEVFCDYSGYAQTSIKTSLTFQSVFKAGKTMRNKLLSVLRLKCHGLFLDLQVNSLQTVCI 992
              |||  ||| ||:|||: ||||   ||||: || ||  ||||||| ||||||||||||||
Db        940 LEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT 999

Qy        993 NIYKIFLLQAYRFHACVIQLPFDQRVRKNLTFFLGIISSQASCCYAILKVKNPGMTLKAS 1052
              ||||| |||||||||:|||| |:| || |||| :||  || ||:||| || ||:| |
Db       1000 NIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAK 1059

Qy       1053 GS---FPPEAAHWLCYQAFLLKLAAHSVIYKCLLGPLRTAQKLLCRKLPEATMTILKAAA 1109
              |:    | ||  |||:|||||||  | | |  ||| |||||  | ||||  |:| |:|||
Db       1060 GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA 1119

Qy       1110 DPALSTDFQTILD 1122
              :||| :||:||||
Db       1120 NPALPSDFKTILD 1132


RESULT 12
AAY26580
ID   AAY26580 standard; protein; 1132 AA.
```

```
XX
AC   AAY26580;
XX
DT   13-SEP-1999  (first entry)
XX
DE   Human telomerase reverse transcriptase (hTERT) enzyme.
XX
KW   Telomerase reverse transcriptase; TERT; mouse; telomere length assay;
KW   immunogen; enzyme; telomerase-mediated DNA replication; human.
XX
OS   Homo sapiens.
XX
PN   WO9927113-A1.
XX
PD   03-JUN-1999.
XX
PF   25-NOV-1998;   98WO-US025211.
XX
PR   26-NOV-1997;   97US-00979742.
PR   16-MAR-1998;   98US-00042460.
XX
PA   (GERO-) GERON CORP.
PA   (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.
XX
PI   Morin GB,  Allsopp R,  Depinho R,  Greenberg R;
XX
DR   WPI; 1999-347722/29.
XX
PT   Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and
PT   nucleic acids.
XX
PS   Disclosure; Fig 3; 135pp; English.
XX
CC   The invention relates to a mouse telomerase reverse transcriptase (mTERT)
CC   enzyme. Compositions containing mTERT can be used in telomere length
CC   assays. Isolated mTERT is useful as an immunogen for the production of
CC   monoclonal or polyclonal antibodies. The method is useful for assessing
CC   the degree of purification and identification of new mTERT species, such
CC   as an mTERT allele, homolog or isoform, or to screen for modulators
CC   (antagonists and agonists) of telomerase-mediated DNA replication.
CC   Antagonists and agonists of mTERT can be used to modify the activity of
CC   other telomerase enzymes such as human TERT (hTERT). The present sequence
CC   represents a human TERT enzyme
XX
SQ   Sequence 1132 AA;

  Query Match             59.4%;  Score 3505;  DB 2;  Length 1132;
  Best Local Similarity   62.4%;  Pred. No. 0;
  Matches  719;  Conservative  122;  Mismatches  260;  Indels   52;  Gaps   13;

Qy          1 MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHW 60
              | ||||| |||||||| |||| ||||||||||:| |||| |||  :| |||||||: |
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR 120
               ::||||  || ||| |||||||||:|||||  :|||||| ||: |||||| |||:|||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA 180
              ||||||| : || |||| ||| |||||:||:||| |||::|| ||||||||| |||| : |
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS 240
                |   |   ||  | | :|         ::  : | :||  || ||: | :|     | |
Db        161 ATQARPPPHAS-GPRRRLG--------CERAWNHSVREAGVPLGLPAPGARRRGGSASRS 231

Qy        241 VPSAKKARCYPVPRVEEGP-------HRQVLPTPSGKSW-VPSPARSPEVPTAEKDLSSK 292
              :|  |: |    |  | |         ||  : : | ||||      ||:  | :
Db        232 LPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPAR-----PAEEATSLE 286

Qy        293 GKVSDLSLS-GSVCCKHKPSSTSLLSPPRQNAFQLRP-FIETRHFLYSRGDGQERLNPSF 350
              | :|    |  ||  :|     |   |||       | : ||:||||| || :|:| |||
Db        287 GALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGD-KEQLRPSF 345

Qy        351 LLSNLQPNLTGARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQY 410
              |||:|:|:|||||||| |||||||    |    | || :|||||||| :|| |||:| |
Db        346 LLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPY 405

Qy        411 VRLLRSHCRFRTANQQVTDAL-----------------NTSPPHLMDLLRLHSSPWQVY 452
                ||::||  | |   || |                 :| |  |: ||| ||||||||
Db        406 GVLLKTHCPLRAA---VTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVY 462

Qy        453 GFLRACLCKVVSASLWGTRHNERRFFKNLKKFISLGKYGKLSLQELMWKMKVEDCHWLRS 512
              ||:|||| ::|   |||:|||||||| :| |||||||: |||||||  ||| | || |||
Db        463 GFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRR 522

Qy        513 SPGKDRVPAAEHRLRERILATFLFWLMDTYVVQLLRSFFYITESTFQKNRLFFYRKSVWS 572
              |||   |||||||||| ||| || |||  |||:||||||:||:|||||||||||||||||
Db        523 SPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWS 582

Qy        573 KLQSIGVRQHLERVRLRELSQEEVRHHQDTWLAMPICRLRFIPKPNGLRPIVNMSYSMGT 632
              ||||||:||||:||:|||||: ||| |::   |:   ||||||||:|||||||| | :|
Db        583 KLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGA 642

Qy        633 RALGRRKQAQHFTQRLKTLFSMLNYERTKHPHLMGSSVLGMNDIYRTWRAFVLRVRALDQ 692
              |    | |:|:  | |:| |||:||||| : | |:|:||||::||:| || |||||||  |
Db        643 RTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDP 702

Qy        693 TPRMYFVKADVTGAYDAIPQGKLVEVVANMIRHSESTYCIRQYAVVRRDSQGQVHKSFRR 752
              | :|||| ||||||| ||| :| ||:|::|:  ::|||:|:||||:: : | |`|:|:
Db        703 PPELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PQNTYCVRRYAVVQKAAHGHVRKAFKS 761

Qy        753 QVTTLSDLQPYMGQFLKHLQDSDASALRNSVVIEQSISMNESSSSLFDFFLHFLRHSVVK 812
              |:||:|||||| ||: |||::  | ||::|||||| |:||:|| ||| || |: |  |:
Db        762 HVSTLTDLQPYMRQFVAHLQET--SPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVR 819

Qy        813 IGDRCYTQCQGIPQGSSLSTLLCSLCFGDMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQ 872
              |  : | |||||||||| ||||||||:||||||||| ::|||||| ||||||||||
Db        820 IRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH 879

Qy        873 AKTFLSTLVHGVPEYGCMINLQKTVVNFPVEPGTLGGAAPYQLPAHCLFPWCGLLLDTQT 932
              ||||| ||| |||||||::||:|||||||||    ||| |  |:||| ||||||||||||:|
Db        880 AKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRT 939

Qy        933 LEVFCDYSGYAQTSIKTSLTFQSVFKAGKTMRNKLLSVLRLKCHGLFLDLQVNSLQTVCI 992
              |||  ||| ||:|||: ||||   ||||: || ||  ||||||| ||||||||||||||
Db        940 LEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT 999

Qy        993 NIYKIFLLQAYRFHACVIQLPFDQRVRKNLTFFLGIISSQASCCYAILKVKNPGMTLKAS 1052
              ||||| |||||||||||:|||| |:| || |||| :||  || ||:||| || ||:| |
Db       1000 NIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAK 1059

Qy       1053 GS---FPPEAAHWLCYQAFLLKLAAHSVIYKCLLGPLRTAQKLLCRKLPEATMTILKAAA 1109
              |:    | ||  |||:|||||||  | | |  ||| |||||  | ||||  |:| |:|||
Db       1060 GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA 1119

Qy       1110 DPALSTDFQTILD 1122
              :||| :||:||||
Db       1120 NPALPSDFKTILD 1132


RESULT 13
AAG64859
ID   AAG64859 standard; protein; 1132 AA.
XX
AC   AAG64859;
XX
DT   21-SEP-2001  (first entry)
XX
DE   Heart muscle cell differentiation related protein SEQ ID NO: 31.
XX
KW   Heart muscle cell; human; cell differentiation; heart disease.
XX
OS   Homo sapiens.
XX
PN   WO200148151-A1.
```

```
XX
PD   05-JUL-2001.
XX
PF   27-DEC-2000; 2000WO-JP009323.
XX
PR   28-DEC-1999;   99JP-00372826.
PR   28-FEB-2000; 2000WO-JP001148.
PR   02-NOV-2000; 2000WO-JP007741.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Umezawa A,  Hata J,  Fukuda K,  Ogawa S,  Sakurada K,  Gojo S;
PI   Yamada Y;
XX
DR   WPI; 2001-425656/45.
DR   N-PSDB; AAH48235.
XX
PT   Cells capable of differentiating into cardiomyocytes and originating in
PT   bone marrow or umbilical blood cells for study of cardiomyocyte
PT   differentiation and treatment of heart disease.
XX
PS   Claim 87; Page 143-147; 183pp; Japanese.
XX
CC   The present invention provides cells originating in the human bone marrow
CC   or umbilical blood cells which are capable of differentiating into
CC   cardiomyocytes. These cells are useful in the treatment of diseases
CC   involving heart muscle degeneration, such as myocardial infarction, and
CC   the study of cardiomyocyte differentiation. The present sequence is a
CC   protein described in the exemplification of the invention
XX
SQ   Sequence 1132 AA;

  Query Match             59.4%;  Score 3505;  DB 4;  Length 1132;
  Best Local Similarity   62.4%;  Pred. No. 0;
  Matches  719;  Conservative  122;  Mismatches  260;  Indels   52;  Gaps   13;

Qy          1 MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHW 60
              | ||||| |||||||| |||| ||||||||||:| |||| ||| :| |||||||: |
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR 120
               ::|||| || ||| |||||||:|||||  :|||||| ||: |||||| |||:|||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA 180
              ||||||| : || |||| ||| ||||||:||:||| |||::|| ||||||||| ||||: |
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS 240
               |   |   ||  | | :|         ::  : | :||  || ||: | :|     | |
Db        181 ATQARPPPHAS-GPRRRLG--------CERAWNHSVREAGVPLGLPAPGARRRGGSASRS 231

Qy        241 VPSAKKARCYPVPRVEEGP-------HRQVLPTPSGKSW-VPSPARSPEVPTAEKDLSSK 292
              :|  |: |    |  |  |       |      || : : | ||||      ||:  | :
Db        232 LPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPAR-----PAEEATSLE 286

Qy        293 GKVSDLSLS-GSVCCKHKPSSTSLLSPPRQNAFQLRP-FIETRHFLYSRGDGQERLNPSF 350
              | :|    |  ||  :|     |   |||       | : ||:||||| || :|:| |||
Db        287 GALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGD-KEQLRPSF 345

Qy        351 LLSNLQPNLTGARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQY 410
              |||:|:|:|||||||| |||||||    |   || :|||||||| :|| |||:| |
Db        346 LLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPY 405

Qy        411 VRLLRSHCRFRTANQQVTDAL-----------------NTSPPHLMDLLRLHSSPWQVY 452
               ||::||  | |  || |                   :| |  |: ||| ||||||||
Db        406 GVLLKTHCPLRAA---VTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVY 462

Qy        453 GFLRACLCKVVSASLWGTRHNERRFFKNLKKFISLGKYGKLSLQELMWKMKVEDCHWLRS 512
              ||:|||| ::|   |||:|||||||| :| ||||||||: |||||||| ||| | || |||
Db        463 GFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRR 522

Qy        513 SPGKDRVPAAEHRLRERILATFLFWLMDTYVVQLLRSFFYITESTFQKNRLFFYRKSVWS 572
              |||   |||||||||| ||| || |||  |||:|||||||:||:|||||||||||||||
Db        523 SPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWS 582

Qy        573 KLQSIGVRQHLERVRLRELSQEEVRHHQDTWLAMPICRLRFIPKPNGLRPIVNMSYSMGT 632
              ||||||:||||:||:|||||: ||| |::   |:  ||||||||:||||||| | :|
Db        583 KLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGA 642

Qy        633 RALGRRKQAQHFTQRLKTLFSMLNYERTKHPHLMGSSVLGMNDIYRTWRAFVLRVRALDQ 692
              |   | |:|:  | |:| |||:||||| : | |:|:||||::||:| || ||||||| |
Db        643 RTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDP 702

Qy        693 TPRMYFVKADVTGAYDAIPQGKLVEVVANMIRHSESTYCIRQYAVVRRDSQGQVHKSFRR 752
              | :|||| ||||||| ||| :| ||:|::|:  ::|||:|:||||:: : | | |:|:
Db        703 PPELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PQNTYCVRRYAVVQKAAHGHVRKAFKS 761

Qy        753 QVTTLSDLQPYMGQFLKHLQDSDASALRNSVVIEQSISMNESSSSLFDPFLHFLRHSVVK 812
              |:||:|||||| ||: |||::  | ||::|||||| |:||:|| ||| || |: |  |:
Db        762 HVSTLTDLQPYMRQFVAHLQET--SPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVR 819

Qy        813 IGDRCYTQCQGIPQGSSLSTLLCSLCFGDMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQ 872
              |  : | |||||||||| |||||||||:||||||||| ::|||||| ||||||||||
Db        820 IRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH 879

Qy        873 AKTFLSTLVHGVPEYGCMINLQKTVVNFPVEPGTLGGAAPYQLPAHCLFPWCGLLLDTQT 932
              ||||| ||| |||||||::||:|||||||||   ||| |  |:||| ||||||||||:|
Db        880 AKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRT 939

Qy        933 LEVFCDYSGYAQTSIKTSLTFQSVFKAGKTMRNKLLSVLRLKCHGLFLDLQVNSLQTVCI 992
              |||  ||| ||:||: ||||   ||||: || ||  ||||||| ||||||||||||||
Db        940 LEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT 999

Qy        993 NIYKIFLLQAYRFHACVIQLPFDQRVRKNLTFFLGIISSQASCCYAILKVKNPGMTLKAS 1052
              ||||| |||||||||||:|||| |:| || |||| :||   || ||:||| || ||:| |
Db       1000 NIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAK 1059

Qy       1053 GS---FPPEAAHWLCYQAFLLKLAAHSVIYKCLLGPLRTAQKLLCRKLPEATMTILKAAA 1109
              |:    | ||  |||:|||||||  | | |  ||| |||||  | ||||  |:| |:|||
Db       1060 GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA 1119

Qy       1110 DPALSTDFQTILD 1122
              :||| :||:|||
Db       1120 NPALPSDFKTILD 1132


RESULT 14
AAG64329
ID   AAG64329 standard; protein; 1132 AA.
XX
AC   AAG64329;
XX
DT   24-SEP-2001  (first entry)
XX
DE   Human protein #2.
XX
KW   Angiogenesis; cardiant; cell differentiating agent; bone marrow;
KW   heart muscle cell; heart disease; human.
XX
OS   Homo sapiens.
XX
PN   WO200148149-A1.
XX
PD   05-JUL-2001.
XX
PF   28-FEB-2000; 2000WO-JP001148.
XX
PR   28-DEC-1999;   99JP-00372826.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Umezawa A,  Hata J,  Fukuda K,  Ogawa S,  Sakurada K;
XX
DR   WPI; 2001-418252/44.
DR   N-PSDB; AAH49601.
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XX
PT   New adult bone marrow-originated cells capable of differentiating into
PT   heart muscle cells, applicable as remedies for various heart diseases
PT   particularly with damaged heart muscle accompanying degeneration.
XX
PS   Disclosure; Page 128-134; 158pp; Japanese.
XX
CC   The present invention relates to cells isolated from bone marrow, which
CC   are capable of at least differentiating into heart muscle cells. The
CC   cells are applicable as remedies for various heart diseases particularly
CC   with damaged heart muscle accompanying degeneration. The present sequence
CC   was used to illustrate the present invention
XX
SQ   Sequence 1132 AA;

  Query Match             59.4%;  Score 3505;  DB 4;  Length 1132;
  Best Local Similarity   62.4%;  Pred. No. 0;
  Matches  719;  Conservative  122;  Mismatches  260;  Indels   52;  Gaps   13;

Qy          1 MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHW 60
              | ||||| |||||||| |||| ||||||||||:| |||| |||  :| ||||||||: |
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR 120
               ::||||  || ||| |||||||:|||||  :|||||| ||: |||||| |||:|||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA 180
              ||||||| : || |||| ||| ||||||:||:||| |||:|| |||||||| |||||: |
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS 240
              |   |   ||  | | :|          ::  : | :||  || ||: | :|      | |
Db        181 ATQARPPPHAS-GPRRRLG--------CERAWNHSVREAGVPLGLPAPGARRRGGSASRS 231

Qy        241 VPSAKKARCYPVPRVEEGP-------HRQVLPTPSGKSW-VPSPARSPEVPTAEKDLSSK 292
              :|  |: |    |  |  |        |      || : : | ||||      ||:  | :
Db        232 LPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPAR-----PAEEATSLE 286

Qy        293 GKVSDLSLS-GSVCCKHKPSSTSLLSPPRQNAFQLRP-FIETRHFLYSRGDGQERLNPSF 350
              | :|    |  ||  :|     |   |||       | : ||:||||| || :|:| |||
Db        287 GALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGD-KEQLRPSF 345

Qy        351 LLSNLQPNLTGARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQY 410
              |||:|:|:||||||||| |||||||   |   |  || :||||||| :|| |||:| |
Db        346 LLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPY 405

Qy        411 VRLLRSHCRFRTANQQVTDAL-----------------NTSPPHLMDLLRLHSSPWQVY 452
                ||::||  | |   || |                  :| |  |: ||| ||||||||
Db        406 GVLLKTHCPLRAA---VTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVY 462

Qy        453 GFLRACLCKVVSASLWGTRHNERRPFKNLKKFISLGKYGKLSLQELMWKMKVEDCHWLRS 512
              ||:|||| ::|   |||:|||||| :| |||||||: |||||| ||| | || |||
Db        463 GFVRACLRRLVPPGLWGSRHNERRPLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRR 522

Qy        513 SPGKDRVPAAEHRLRERILATFLFWLMDTYVVQLLRSFFYITESTFQKNRLFFYRKSVWS 572
              |||   |||||||||| ||| || |||  |||:|||||||:||:|||||||||||||||
Db        523 SPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWS 582

Qy        573 KLQSIGVRQHLERVRLRELSQEEVRHHQDTWLAMPICRLRFIPKPNGLRPIVNMSYSMGT 632
              ||||||:||||:||:|||||: ||| |::   |:   ||||||||:|||||||| | :|
Db        583 KLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGA 642

Qy        633 RALGRRKQAQHFTQRLKTLFSMLNYERTKHPHLMGSSVLGMNDIYRTWRAFVLRVRALDQ 692
              |   | |:|:  | |:| |||:|||||  : | |:|:||||::||:| || |||||||  |
Db        643 RTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDP 702

Qy        693 TPRMYFVKADVTGAYDAIPQGKLVEVVANMIRHSESTYCIRQYAVVRRDSQGQVHKSFRR 752
              | :|||| ||||||| ||| :| ||:|::|:  ::|||:|:||||:: : | |:|:
Db        703 PPELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PQNTYCVRRYAVVQKAAHGHVRKAFKS 761

Qy        753 QVTTLSDLQPYMGQFLKHLQDSDASALRNSVVIEQSISMNESSSSLFDFFLHFLRHSVVK 812
                |:||:|||||| ||: |||::  | ||::|||||| |:||:|| ||| || |: |  |:

Db        762 HVSTLTDLQPYMRQFVAHLQET--SPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVR 819

Qy        813 IGDRCYTQCQGIPQGSSLSTLLCSLCFGDMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQ 872
              |  : | ||||||||| |||||||||:|||||||| ::||||||| ||||||||||
Db        820 IRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH 879

Qy        873 AKTFLSTLVHGVPEYGCMINLQKTVVNFPVEPGTLGGAAPYQLPAHCLFPWCGLLLDTQT 932
              ||||| ||| |||||||::||:|||||||||    ||| |  |:||| ||||||||||:|
Db        880 AKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRT 939

Qy        933 LEVFCDYSGYAQTSIKTSLTFQSVFKAGKTMRNKLLSVLRLKCHGLFLDLQVNSLQTVCI 992
              |||  ||| ||:|||: ||||   ||||: || ||  ||||||| ||||||||||||||
Db        940 LEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT 999

Qy        993 NIYKIFLLQAYRFHACVIQLPFDQRVRKNLTFFLGIISSQASCCYAILKVKNPGMTLKAS 1052
              ||||| ||||||||||:|||| |:| || |||| :||  || ||:||| || ||:| |
Db       1000 NIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAK 1059

Qy       1053 GS---FPPEAAHWLCYQAFLLKLAAHSVIYKCLLGPLRTAQKLLCRKLPEATMTILKAAA 1109
              |:    | ||  |||:|||||||  | | |  ||| |||||  | ||||  |:| |:|||
Db       1060 GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA 1119

Qy       1110 DPALSTDFQTILD 1122
              :||| :||:||||
Db       1120 NPALPSDFKTILD 1132


RESULT 15
AAB99930
ID   AAB99930 standard; protein; 1132 AA.
XX
AC   AAB99930;
XX
DT   26-SEP-2001  (first entry)
XX
DE   Human telomerase protein sequence SEQ ID NO:31.
XX
KW   Differentiation; heart muscle cell; cytokine; transcription factor;
KW   proliferation; surface antigen; heart disease; cardiomyocyte;
KW   bone marrow; umbilical blood cell; heart muscle degeneration;
KW   myocardial infarction.
XX
OS   Homo sapiens.
XX
PN   WO200148150-A1.
XX
PD   05-JUL-2001.
XX
PF   02-NOV-2000; 2000WO-JP007741.
XX
PR   28-DEC-1999;   99JP-00372826.
PR   28-FEB-2000; 2000WO-JP001148.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Umezawa A,  Hata J,  Fukuda K,  Ogawa S,  Sakurada K,  Gojo S;
PI   Yamada Y;
XX
DR   WPI; 2001-425655/45.
DR   N-PSDB; AAH44366.
XX
PT   Cells capable of differentiating into cardiomyocytes and originating in
PT   bone marrow or umbilical blood cells for study of cardiomyocyte
PT   differentiation and treatment of heart disease.
XX
PS   Claim 146; Page 137-141; 187pp; Japanese.
XX
CC   The present invention describes cells originating in bone marrow or
CC   umbilical blood cells which are capable of differentiating into
CC   cardiomyocytes. Also described are: (1) cardiomyocytes produced by the
CC   differentiation of the cells; (2) a method for carrying out the
CC   differentiation into cardiomyocytes, regulated by a promotional and/or
CC   inhibitory factor; (3) a method for the differentiation of the cells into
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CC cell types other than cardiomyocytes; (4) drug compositions promoting the
CC formation of heart muscle and regeneration of heart tissue which contain
CC the cells; (5) a method for the production of antibodies which recognise
CC the cells, especially antibodies which recognise a surface antigen on the
CC cells; (6) a method for screening factors which promote the proliferation
CC of the cells; (7) a method for immortalising the cells by expressing
CC telomerase in them; (8) drug compositions for the treatment of heart
CC disease which contain the immortalised cells; and (9) cell-free
CC supernatant from the culture of the cells and its use in promoting their
CC differentiation into cardiomyocytes. The cells are used in the treatment
CC of diseases involving heart muscle degeneration, such as myocardial
CC infarction and in the study of cardiomyocyte differentiation. AAH44351 to
CC AAH44409 and AAB99915 to AAB99935 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 1132 AA;

Query Match 59.4%; Score 3505; DB 4; Length 1132;
Best Local Similarity 62.4%; Pred. No. 0;
Matches 719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;

```
Qy          1 MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHW 60
              | ||||| |||||||| |||| ||||||||||:| |||| ||| :| ||||||||: |
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR 120
               ::|||| || ||| ||||||||:|||||| :||||||| ||: |||||| |||:|||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA 180
              ||||||| : || |||| ||| |||||:||:||| |||::|| ||||||||| ||||: |
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS 240
                |   |   ||  | | :|         ::  : | :||  || ||: | :|     | |
Db        181 ATQARPPPHAS-GPRRRLG--------CERAWNHSVREAGVPLGLPAPGARRRGGSASRS 231

Qy        241 VPSAKKARCYPVPRVEEGP-------HRQVLPTPSGKSW-VPSPARSPEVPTAEKDLSSK 292
              :|  |: |    |  |  |       |      || : : | ||||      ||:  | :
Db        232 LPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPAR-----PAEEATSLE 286

Qy        293 GKVSDLSLS-GSVCCKHKPSSTSLLSPPRQNAFQLRP-FIETRHFLYSRGDGQERLNPSF 350
              | :|   | || :|     |  |||       | : ||:||||| || :|:| |||
Db        287 GALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGD-KEQLRPSF 345

Qy        351 LLSNLQPNLTGARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQY 410
              |||:|:|:|||||||| |||||||    |   | || :|||||||| :|| |||:| |
Db        346 LLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPY 405

Qy        411 VRLLRSHCRFRTANQQVTDAL------------------NTSPPHLMDLLRLHSSPWQVY 452
                ||::||  | |   || |                   :| |  |: ||| ||||||||
Db        406 GVLLKTHCPLRAA---VTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVY 462

Qy        453 GFLRACLCKVVSASLWGTRHNERRFFKNLKKFISLGKYGKLSLQELMWKMKVEDCHWLRS 512
              ||:|||| ::|   |||:||||||| :| |||||||: ||||||| ||| | || |||
Db        463 GFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRR 522

Qy        513 SPGKDRVPAAEHRLRERILATFLFWLMDTYVVQLLRSFFYITESTFQKNRLFFYRKSVWS 572
              |||   |||||||||| ||| || |||  |||:|||||||:||:|||||||||||||||
Db        523 SPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWS 582

Qy        573 KLQSIGVRQHLERVRLRELSQEEVRHHQDTWLAMPICRLRFIPKPNGLRPIVNMSYSMGT 632
              ||||||:||||:||:|||||: ||| |::   |:   ||||||||:|||||||| | :|
Db        583 KLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGA 642

Qy        633 RALGRRKQAQHFTQRLKTLFSMLNYERTKHPHLMGSSVLGMNDIYRTWRAFVLRVRALDQ 692
              |   | |:|:  | |:| |||:||||| : | |:|:||||::||:| || ||||||| |
Db        643 RTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDP 702

Qy        693 TPRMYFVKADVTGAYDAIPQGKLVEVVANMIRHSESTYCIRQYAVVRRDSQGQVHKSFRR 752
              | :|||| ||||||| ||| :| ||:|::|:  ::|||:|:||||:: : | | |:|:
Db        703 PPELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PQNTYCVRRYAVVQKAAHGHVRKAFKS 761

Qy        753 QVTTLSDLQPYMGQFLKHLQDSDASALRNSVVIEQSISMNESSSSLFDFFLHFLRHSVVK 812
              |:||:|||||| ||: |||::  | ||::|||||| |:||:|| ||| || |: |  |:
Db        762 HVSTLTDLQPYMRQFVAHLQET--SPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVR 819

Qy        813 IGDRCYTQCQGIPQGSSLSTLLCSLCFGDMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQ 872
              |  : | ||||||||| |||||||||:||||||||| ::|||||| ||||||||||
Db        820 IRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH 879

Qy        873 AKTFLSTLVHGVPEYGCMINLQKTVVNFPVEPGTLGGAAPYQLPAHCLFPWCGLLLDTQT 932
              ||||| ||| |||||||::||:|||||||||    ||| |  |:||| ||||||||||:|
Db        880 AKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRT 939

Qy        933 LEVFCDYSGYAQTSIKTSLTFQSVFKAGKTMRNKLLSVLRLKCHGLFLDLQVNSLQTVCI 992
              |||  ||| ||:|||: ||||   ||||: || ||  ||||||| ||||||||||||||
Db        940 LEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT 999

Qy        993 NIYKIFLLQAYRFHACVIQLPFDQRVRKNLTPFLGIISSQASCCYAILKVKNPGMTLKAS 1052
              ||||| ||||||||||:|||| |:| || |||| :||  || ||:||| || ||:| |
Db       1000 NIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAK 1059

Qy       1053 GS---FPPEAAHWLCYQAFLLKLAAHSVIYKCLLGPLRTAQKLLCRKLPEATMTILKAAA 1109
              |:   | ||  |||:|||||  | | |  ||| ||||  | ||||  |:| |:|||
Db       1060 GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA 1119

Qy       1110 DPALSTDFQTILD 1122
              :||| :||:|||| 
Db       1120 NPALPSDFKTILD 1132
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Search completed: May 15, 2006, 13:30:22
Job time : 196 secs